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Qy	901	GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCACGAGACTGAGACATATCTGCACCTC	960
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DEFINITION Sequence 1 from patent US 5981711..
ACCESSION AR085316
VERSION AR085316.1 GI:10012085
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (Bases 1 to 1522)
TITLES Zavada,J., Pastorekova,S. and Pastorek,J.
JOURNAL MN-specific antibodies and hybridomas
Patent: US 5981711-A 1 09-NOV-1999;
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Db	61	CTGTGCTCAGGGCTTCATCTGTGCCAATCTGTGTGTCTCATCTGTGCTTCTTGAGGCTGTGCAT	120	
QY	121	CCCCAGAGAGTTGCCCCGGATGACAGAGAAATCCCCCTTGAGAGAGAGCTCTTCTGAGGAA	180	
Db	121	CCCCAGAGAGTTGCCCCGGATGACAGAGAAATCCCCCTTGAGAGAGAGCTCTTCTGAGGAA	180	
QY	181	GATGACCACTGTGGCGAGAGAGATCTGCCCCAGTGAAGAGATTCAACCAGAGAGAGAT	240	
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QY	241	CCACCCCGAGAGAGAGATCTACCTGTGAGAGAGAGATCTACCTGTGAGAGAGAGATCTACCT	300	
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QY	301	GAAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGT	360	
Db	301	GAAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGT	360	
QY	361	GAGGCTCTTGAGAGATCTCTCAAGAACCCCGAATATGTCCCAAGAGACAAAGAGGGAT	420	
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QY	541	CTGTGCCCCCTTGGAACTCTGTGGCTTCCAGCTCCGCGCTCCCAAGACTGTGGCTGTGC	600	
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QY	661	GGGGGGAGTACCGGGGCTGTGACGTGCACTGTGAGCTGTGGGGGCTGTGACGTCGTCGGGC	720	
Db	661	GGGGGGAGTACCGGGGCTGTGACGTGCACTGTGAGCTGTGGGGGCTGTGACGTCGTCGGGC	720	
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DEFINITION Sequence 1 from patent US 5989838.
ACCESSION AR088064
VERSION AR088064.1 GI:10014827
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 1 23-NOV-1999;
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LOCUS Definition Sequence 1 from patent US 6093548.
ACCESSION ARI04223
VERSION ARI04223.1 GI:12816931
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 1 25-JUL-2000;
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DEFINITION Sequence 1 from patent US 6204370.
ACCESSION ARI43487
VERSION ARI43487.1 GI:15104773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 1 20-MAR-2001;
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ACCESSION AR171392
VERSION AR171392.1 GI:17910342
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 1 02-OCT-2001;
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DEFINITION Sequence 1 from patent US 6297051.
ACCESSION AR171563
VERSION AR171563.1 GI:17910513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE MN gene and protein
JOURNAL Patent: US 6297051-A 1 02-OCT-2001;
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ORGANISM Homo sapiens
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Zavada,J., Pastorekova,S. and Pastorek,J.
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REFERENCE
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Aistle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J.,
Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.E., Malmonts, P.J.,
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and
Molino, G.A.
Detection methods using T1P 1 for colon cancer diagnosis
Patent: EP 1439393-A 71 21-JUL-2004;
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
AND RESEARCH (US)

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source location/Qualifiers
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
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DEFINITION Sequence 516 from Patent WO0194629.
ACCESSION AX330007
VERSION AX330007.1 GI:18102985
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Young, P.B., Augustus, M., Carter, K.C., Ehner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 516 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Db 1531 TTTTAAATTAATTTATTAAT 1552

RESULT 12
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LOCUS AX332607 1552 bp DNA linear PAT 09-JUN-2002
DEFINITION Sequence 3116 from Patent WO0194629.
ACCESSION AX332607
VERSION AX332607.1 GI:18123241
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Young, P.B., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)
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RESULT 14
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LOCUS AX336174 Sequence 6683 from Patent WO0194629.
DEFINITION AX336174
ACCESSION AX336174.1 GI:18126893
VERSION

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 6683 13-DEC-2001;
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RESULT 15
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DEFINITION   H.sapiens Matu MN mRNA for p54/58n protein.
ACCESSION    X66839
VERSION      X66839.1 GI:1000701
KEYWORDS     transmembrane glycoprotein.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE    1 (bases 1 to 1552)
AUTHORS      Pastorek,J.
TITLE        Direct Submission
JOURNAL      Submitted (11-JUN-1992) J. Pastorek, Institute of Virology, Slovak
REPUBLIC     Academy of Sciences, Dubravka 9, 842 46 Bratislava, SLOVAK
REMARK       revised by [3] MAT

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REFERENCE    2 (bases 1 to 1552)
AUTHORS      Pastorek,J., Pastorekova,S., Callebaut,I., Mornon,J., Zelink,V.,
Opavsky,R., Zatojicova,M., Liao,S., Portetle,D., Stanbridge,E.J.,
Zavada,J. and Burny,A.
TITLE        Cloning and characterization of MN, a human tumor-associated
protein with a domain homologous to carbonic anhydrase and a
putative helix-loop-helix DNA binding segment
JOURNAL      Oncogene 9 (10), 2877-2888 (1994)
MEDLINE      9436734
PUBMED       8084592
REFERENCE    3 (bases 1 to 1552)
AUTHORS      Pastorek,J.
TITLE        Direct Submission
JOURNAL      Submitted (19-JUN-1994) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Dubravka 9, 842 46 Bratislava, SLOVAK
REPUBLIC
REMARK       revised by [4] MAT
AUTHORS      Pastorek,J.
TITLE        Direct Submission
JOURNAL      Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Dubravka 9, 842 46 Bratislava, SLOVAK
REPUBLIC
COMMENT      On Sep 29, 1995 this sequence version replaced gi:558593.
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        Query Match      100.0%; Score 1522; DB 9; Length 1552;
        Best Local Similarity 100.0%; Pred. No. 0;
        Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 6, 2005, 09:33:20
 Job time : 6359 secs

XX MN gene, protein and nucleic acid fragments - used as primers and probes
PT in the detection of MN antigens and antibodies, and in the treatment of
PT (pre)neoplastic disease.

PS Claim 1, Fig 1, 102pp: English.

XX The present sequence is the full length Mutu endogenous cellular
CC component, MN, cDNA clone, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the
CC exogenous Mutu transmissible agent (MX), infection increases the
CC expression level of the MN gene. MN is a putative oncogene, and can
CC therefore be used in the development of probes for the diagnosis and
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC vaccine contg. immunogenic amounts of the MN protein can be used to
CC immunise a vertebrate against a NP disease associated with MN antigen
CC expression. (updated on 25-MAR-2003 to correct PR field.)

XX Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 2; Length 1522;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1501 TTTTAAATTAATTTTAAAT 1522

RESULT 2
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XX AA16540;
AC 16-JUN-2000 (first entry)
XX
XX
DE Human MN protein encoding cDNA SEQ ID NO:1.
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KM oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW MN/CA IX isoenzyme; ds.
XX
OS Homo sapiens.

XX US6027887-A.
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XX Pastorek J, Zavada J, Pastorekova S;
XX WPI, 2000-194827/17.
XX P-PSDB, AAY53228.
XX Nucleic acid based assay for diagnosing a wide variety of
XX preneoplastic/neoplastic disease comprises screening for the presence of
XX abnormal MN gene expression in a vertebrate.
XX Claim 1, Fig 1, 87pp, English.
XX The present invention describes a method of screening for
XX preneoplastic/neoplastic disease. The method comprises: (1) determining
XX whether abnormal MN gene expression is present in a vertebrate; and (2)
XX if abnormal MN gene expression is determined to be present in the
XX vertebrate, determining that the vertebrate has a significant risk of
XX having preneoplastic/neoplastic disease. The MN gene is an oncogene and
XX encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
XX protein is a tumour associated carbonic anhydrase isoenzyme. The method
XX is used for detecting a wide variety of preneoplastic/neoplastic diseases
XX in a vertebrate, preferably a human. The disease detected is mammary,
XX bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
XX testicular, brain, head and neck, mesodermal, gallbladder, rectal,
XX duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
XX mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
XX mucosa, pancreatic duct epithelium or liver duct epithelium
XX preneoplastic/neoplastic disease. AAI16540 to AAI16617 and AAY53228 to
XX AAY53245 represent sequences used in the exemplification of the present
XX invention.
XX Sequence 1522 BP, 297 A, 458 C, 453 G, 314 T, 0 U, 0 Other;
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Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 CCGTGCACGAGGCTCACTGTCGAACGCTGCTGTCATCTGCTTGTGATCCGACC 120
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DB 121 CCCGACGAGGTTGCCCGAGATGACAGAGATTCCCTTGGAGAGAGGCTTTCTGGAGAA 180
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DB 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240

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DB 781 ACCGCTTTGCAAGATTGACAGAGGCTTGGAGGCGCCGAGAGGCTGAGGCTGTTGGCC 840
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DB 1261 GCGCTGATTTTGGCTCTTTTGTGTCACCAAGGCTGCTTCTTGTGAGATGAGA 1320
QY 1321 AGGCAAGCAAGAAAGGGAACCAAGAGGAGTGTGAGCTACCGCCAGAGAGTACGCGAG 1380

Dd		1321	AGGACGACAGAAAGGGGAACCAAGAGGGGTGTGAGCTACCGCCACGACGAGAAGTATGCCAG	1380
Gy		1361	ACTGGAAGCCTTAGAGCTTGATCTTTGGAGAAATGTGAGAAAGCCAGACGACATCTGAGGG	1440
Dd		1361	ACTGAGGCTTAGAGGCTGGATCTTGGAAATGTGAGAAAGCCAGCCAGAGCATCTGAGGG	1440
Gy		1441	GGAGCCGGTAACTGTCCTGTCCTGCATTATNGCACTTCCTTTAATCTGCCAAGAAATT	1500
Dd		1441	GGAGCCGGTAACTGTCCTGTCCTGCATTATNGCACCTTCCTTTAATCTGCCAAGAAATT	1500
Gy		1501	TTTTTAATAATAATATTATTAAT	1522
Dd		1501	TTTTTAATAATAATATTATTAAT	1522
<hr/>				
RESULT 3				
AAAS2459				
ID	AAAS2459	standard; cDNA; 1522 BP.		
XX				
AC	AAAS2459;			
DT	25-SEP-2000	(first entry)		
XX				
DE	Human MN CDNA.			
KM	MN protein; tumor associated cell adhesion molecule; oncoprotein;			
KW	proteoglycan domain; PG domain; carbonic anhydrase; CA domain;			
KV	abnormal expression; neoplastic disease; cancer; gene therapy; ss.			
XX				
OS	Homo sapiens.			
FH		Location/Qualifiers		
FT	CDS	13..1392		
FT		/tag= a		
FT		/product= "Human MN protein"		
XX				
PN	WO200024913-A2.			
XX				
PD	04-MAY-2000.			
XX				
PF	22-OCT-1999;	99WO-US024879.		
XX				
PR	23-OCT-1998;	98US-00177776.		
PR	23-OCT-1998;	98US-00178115.		
PA	(FARB) BAYER CORP.			
PA	(VIRO-) INST VIROLOGY.			
XX				
PI	Zavada J, Pastorekova S, Pastorek J;			
DR	WPI; 2000-350752/30.			
DR	P-PADB; AAB03005.			
PT				
PT	A molecule which specifically binds to a site on MN protein (oncoprotein)			
PT	and prevents adhesion of vertebrate cells to the protein, useful for			
XX	treating preneoplastic or neoplastic diseases such as cancer.			
XX				
PS	Example 1; Fig 1A-C; 154pp; English.			
CC	The invention relates to the inhibition of cell adhesion mediated by the			
CC	MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G25O			
CC	protein). The MN protein is a tumour-associated adhesion molecule which			
CC	comprises a proteoglycan-like (PG) domain (AAB03017) which contains the			
CC	protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).			
CC	Abnormal expression of the MN protein is associated with tumorigenicity.			
CC	The invention encompasses molecules (e.g., proteins and peptides) which			
CC	specifically bind to a site on the MN protein, thereby preventing			
CC	adhesion of vertebrate cells to the protein in a cell adhesion assay. It			
CC	also encompasses MN proteins or MN protein fragments which can be added			
CC	to the extracellular environment to prevent the adhesion of vertebrate			
CC	cells to each other. The invention also relates to the identification of			
CC	the binding site of the MN protein and to a method of identifying a site			

CC	on an MN protein to which cells adhere, comprising testing a series of
CC	overlapping peptides from the protein in a cell adhesion assay. The
CC	invention encompasses a vector comprising an expression control sequence
CC	operatively linked to a nucleic acid encoding the variable domains of a
CC	MN-specific antibody, where the domains are separated by a flexible
CC	linker peptide (AAB83035) and the vector inhibits the growth of a
CC	vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC	protein. The invention also encompasses a vector comprising a nucleic
CC	acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC	gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC	neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC	gene promoter (AA52473). MN proteins and peptides, MN-binding proteins
CC	and peptides, and expression vectors encoding such proteins and peptides
CC	are useful for treating patients with preneoplastic or neoplastic disease
CC	(e.g., cancers) associated with or characterized by abnormal MN
CC	expression. The present sequence represents cDNA encoding the human MN
CC	protein
CC	
XX	
SQ	Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
Query Match	100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1522;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dy	1 ACAGTCAAGCCGATAGCTCCCCCTTGCCGCCACCCCTGGCTCCTCTTGTGATCCCGGC 60
Db	1 ACAGTCAAGCCGATAGCTCCCCCTTGCCGCCACCCCTGGCTCCTCTTGTGATCCCGGC 60
Dy	61 CTGCTCCAGGCCCCTCATCTGTCGAACCTGTGTGTCATCTGTCGTTTCTGATCCTGTCAT 120
Db	61 CTGCTCCAGGCCCCTCATCTGTCGAACCTGTGTGTCATCTGTCGTTTCTGATCCTGTCAT 120
Dy	121 CCCGAGAATTGCCCGGATGACAGAGGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGGA 180
Dy	121 CCCGAGAATTGCCCGGATGACAGAGGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGGA 180
Db	121 CCCGAGAATTGCCCGGATGACAGAGGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGGA 180
Dy	181 GATTAATCCACTGCGGCGAGAGAGATCTGCCCAGTGAAGAGATTCAACCAGAGAGAGAT 240
Dy	181 GATTAATCCACTGCGGCGAGAGAGATCTGCCCAGTGAAGAGATTCAACCAGAGAGAGAT 240
Db	181 GATTAATCCACTGCGGCGAGAGAGATCTGCCCAGTGAAGAGATTCAACCAGAGAGAGAT 240
Dy	241 CCACCCGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCT 300
Dy	241 CCACCCGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCT 300
Db	241 CCACCCGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCTGGAGAGAGAGATCTAACCT 300
Dy	301 GAAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAATACTGT 360
Dy	301 GAAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAATACTGT 360
Db	301 GAAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAATACTGT 360
Dy	361 GAAGCTCTTGGAGATCTTCAAGAACCCCAAGATATAGCCACAAGAGACAAAGAGGGAT 420
Dy	361 GAAGCTCTTGGAGATCTTCAAGAACCCCAAGATATAGCCACAAGAGACAAAGAGGGAT 420
Db	361 GAAGCTCTTGGAGATCTTCAAGAACCCCAAGATATAGCCACAAGAGACAAAGAGGGAT 420
Dy	421 GACCAAGTCAATTGACGCTATGAGAGGACCCGCGCTGCGCCCGGATGTCCCAAGCCTGC 480
Dy	421 GACCAAGTCAATTGACGCTATGAGAGGACCCGCGCTGCGCCCGGATGTCCCAAGCCTGC 480
Db	421 GACCAAGTCAATTGACGCTATGAGAGGACCCGCGCTGCGCCCGGATGTCCCAAGCCTGC 480
Dy	481 GCGGCGCGCTTCCAAGTCCCGGATGATATCCGCCCAAGCTCGCGGCTTCTGCCCCGCC 540
Dy	481 GCGGCGCGCTTCCAAGTCCCGGATGATATCCGCCCAAGCTCGCGGCTTCTGCCCCGCC 540
Db	481 GCGGCGCGCTTCCAAGTCCCGGATGATATCCGCCCAAGCTCGCGGCTTCTGCCCCGCC 540
Dy	541 CTGCGCCCCCTGGAACCTCTGGGGTTCCAAGTCCCGCGCTCCCAAGACTGCGGCTGGGC 600
Dy	541 CTGCGCCCCCTGGAACCTCTGGGGTTCCAAGTCCCGCGCTCCCAAGACTGCGGCTGGGC 600
Db	541 CTGCGCCCCCTGGAACCTCTGGGGTTCCAAGTCCCGCGCTCCCAAGACTGCGGCTGGGC 600
Dy	601 AACATATGACCAAGTGTGCACTGACCTCTGCGCTCTTGGGCTTAGAGATGCTTGGGATCCC 660
Dy	601 AACATATGACCAAGTGTGCACTGACCTCTGCGCTCTTGGGCTTAGAGATGCTTGGGATCCC 660
Db	601 AACATATGACCAAGTGTGCACTGACCTCTGCGCTCTTGGGCTTAGAGATGCTTGGGATCCC 660
Dy	661 GGCGGGAGATACCGGGGCTTGCAGCTGCACTGTGACCTGGGGAGGTGCAAGTGTCCGGGC 720
Dy	661 GGCGGGAGATACCGGGGCTTGCAGCTGCACTGTGACCTGGGGAGGTGCAAGTGTCCGGGC 720
Db	661 GGCGGGAGATACCGGGGCTTGCAGCTGCACTGTGACCTGGGGAGGTGCAAGTGTCCGGGC 720
Dy	721 TCAGAGCACTGTGAAGGCAACGTTTTCTTCCGAGATCCACGTGTTCACCTCAGC 780

```
Db 721 TCGAGACACACTGTGAGAGCCACCGTTTCCCTGCCGAGATCAGCTGGTTACCTCAGC 780
Qy 781 ACCGCTTTTCCAGAGTTGACGAGGCTTTGGGGCGCCGGAGAGGCTGGCCGTGTGGCC 840
Db 781 ACCGCTTTTCCAGAGTTGACGAGGCTTTGGGGCGCCGGAGAGGCTGGCCGTGTGGCC 840
Qy 841 GCTTTCTGAGAGAGGCGCCGGAGAGAAACAGTGCCTATGAGAGATTGCTGTGCTGGCTG 900
Db 841 GCTTTCTGAGAGAGGCGCCGGAGAGAAACAGTGCCTATGAGAGATTGCTGTGCTGGCTG 900
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGCTGAGCATATCTGCACTC 960
Db 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGCTGAGCATATCTGCACTC 960
Qy 961 CTGCTCTGAGATTGAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGT 1020
Db 961 CTGCTCTGAGATTGAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGT 1020
Qy 1021 GCCCAGGGTGTGATCTGAGCTGTGTTAACAGACAGTATGCTGATGCTTAAGCAGCTC 1080
Db 1021 GCCCAGGGTGTGATCTGAGCTGTGTTAACAGACAGTATGCTGATGCTTAAGCAGCTC 1080
Qy 1081 CACACCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGA 1140
Db 1081 CACACCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGA 1140
Qy 1141 GCGAGCGACGCTTTGAAATGGGGAGTGAATTGAGGCTCTCTCTGCTGAGTGAAGCAGC 1200
Db 1141 GCGAGCGACGCTTTGAAATGGGGAGTGAATTGAGGCTCTCTCTGCTGAGTGAAGCAGC 1200
Qy 1201 AGTCCTCGGGGCTGTGAGGCACTGAGTCCAGTGAATTCCTGCTGGCTGCTGAGATCCCTA 1260
Db 1201 AGTCCTCGGGGCTGTGAGGCACTGAGTCCAGTGAATTCCTGCTGGCTGCTGAGATCCCTA 1260
Qy 1261 GGCCTGTGTTTGGCCCTCTTTTGTGCTGACACAGGCTGCGCTTCTCTGAGATGAGA 1320
Db 1261 GGCCTGTGTTTGGCCCTCTTTTGTGCTGACACAGGCTGCGCTTCTCTGAGATGAGA 1320
Qy 1321 AGGCGACACAGAAAGGGGAAACAAAGGGGCTGTGAGTACCCGCCAGCAGAGGTAAGCCGAG 1380
Db 1321 AGGCGACACAGAAAGGGGAAACAAAGGGGCTGTGAGTACCCGCCAGCAGAGGTAAGCCGAG 1380
Qy 1381 ACTGAGGCTTGAAGGCTGTGATCTTGAGATGTGAGAGCCAGCCAGAGGCAATCTGAGGG 1440
Db 1381 ACTGAGGCTTGAAGGCTGTGATCTTGAGATGTGAGAGCCAGCCAGAGGCAATCTGAGGG 1440
Qy 1441 GGAGCGGTAACTGTCTGTCTGCTCATTAATGCCACTTCTTTTAACCTGCCAAGAAATT 1500
Db 1441 GGAGCGGTAACTGTCTGTCTGCTCATTAATGCCACTTCTTTTAACCTGCCAAGAAATT 1500
Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1501 TTTTAAATTAATTAATTAAT 1522

RESULT 4
ADG31413
ID ADG31413 standard; cDNA; 1522 BP.
XX AC ADG31413;
XX XX
XX 26-FEB-2004 (first entry)
XX DE Human MN cDNA SeqID 1.
XX XX
XX human; gene; ss; monoclonal antibody; MN/CA IX; MN; oncogene;
XX KM carbonic anhydrase 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
XX KM neoplastic tumour; cytostatic; cancer; tumour therapy;
XX KM anti-tumour vaccine.
XX OS Homo sapiens.
XX XX
```

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PN WO2003100029-A2.
XX
PD 04-DEC-2003.
XX
PF 22-FEB-2003; 2003WO-US005136.
XX
PR 23-MAY-2002; 2002US-0383068P.
XX 05-DEC-2002; 2002US-0431499P.
XX
PA (FARB ) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
XX
PI Pastorek J, Pastorekova S, Zatoricova M, Zavada J, Orlova Gut M;
XX WPI: 2004-035136/03.
XX P-PSDB; ADG31414.
XX
PT New monoclonal antibody generated from MN/CA IX-deficient mice, where the
PT antibody binds specifically to human tumor-associated cell adhesion
PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 1; 156pp; English.
XX
CC This invention relates to a novel monoclonal antibody identified as the
CC MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
CC mice). Specifically, this antibody is directed towards the MN gene, a
CC cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC present invention describes the generation of this monoclonal antibody,
CC and immunoreactive fragments thereof, which are directed against non-
CC immunodominant epitopes on the CA IX extracellular domain. As such, this
CC antibody can be useful diagnostically as a marker for preneoplastic/
CC neoplastic tumours, immunodetection methods and immunotargeting
CC approaches. Accordingly, compositions exhibit cytostatic activity and are
CC useful in the diagnosis, prognosis and treatment of various cancers
CC including breast, bladder or lung cancer, in tumour therapy and in anti-
CC tumour vaccination. This polynucleotide sequence is the human MN cDNA of
CC the invention.
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 1522; DB 12; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACAGTCAGCCGATGAGTCCCTGTCGCCAGCCCTGGCTCCCTGTGATCCCGGCC 60
Db 1 ACAGTCAGCCGATGAGTCCCTGTCGCCAGCCCTGGCTCCCTGTGATCCCGGCC 60
Qy 61 CCTGCTCCAGGCTCACTGTGTCACTGTGTCACTGTGTCTGTGATGCTGTCAAT 120
Db 61 CCTGCTCCAGGCTCACTGTGTCACTGTGTCACTGTGTCTGTGATGCTGTCAAT 120
Qy 121 CCCGAGGTTGGCCCGGATGAGAGATTCCTCCCTTGGAGAGGCTTCTGTGGGAA 180
Db 121 CCCGAGGTTGGCCCGGATGAGAGATTCCTCCCTTGGAGAGGCTTCTGTGGGAA 180
Qy 181 GATGACCCACTGTGGGAGAGAGATCTGCCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
Db 181 GATGACCCACTGTGGGAGAGAGATCTGCCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
Qy 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
Db 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
Qy 301 GAAGTTAAGCCCTAAATCGAAGAAGAGGCTCCGAGATTGAGAGATCTACTGTGTT 360
Db 301 GAAGTTAAGCCCTAAATCGAAGAAGAGGCTCCGAGATTGAGAGATCTACTGTGTT 360
Qy 361 GAGGCTCCTGAGATCTCAAGAACCCAGAAATTAATGCCAGAGGAGCAAGAGAGGAGAT 420
Db 361 GAGGCTCCTGAGATCTCAAGAACCCAGAAATTAATGCCAGAGGAGCAAGAGAGGAGAT 420
```

Db 361 GAGGCTCTGGAGATCTCAAGAACCCGAGATATATGCCACAGGGACAAAGAGGGGAT 420
Qy 421 GACAGAGTCAATTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGCCAGGCTGC 480
Db 421 GACAGAGTCAATTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGCCAGGCTGC 480
Qy 481 GGGGGGCGCTTCCAGTCCCGGTGGATATCCCGCCCACTGGCCGCTTTCGCCGACC 540
Db 481 GGGGGGCGCTTCCAGTCCCGGTGGATATCCCGCCCACTGGCCGCTTTCGCCGACC 540
Qy 541 CTGGCGCCCTGGAGATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGC 600
Db 541 CTGGCGCCCTGGAGATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGC 600
Qy 601 AACATGSCCAAGTGTGCACTGACCTGCTCTCTGGGCTAGAGATGCTGTGGGTCCC 660
Db 601 AACATGSCCAAGTGTGCACTGACCTGCTCTCTGGGCTAGAGATGCTGTGGGTCCC 660
Qy 661 GGGGGGAGTACCGGGCTCTGAGCTGTGCACTGTGGGAGGCTGTGCAAGTGTCCGGGC 720
Db 661 GGGGGGAGTACCGGGCTCTGAGCTGTGCACTGTGGGAGGCTGTGCAAGTGTCCGGGC 720
Qy 721 TCGAGACACTGTGAGAGGCCACCGTTCCTGCGAGATCAAGTGTCACTCAAGC 780
Db 721 TCGAGACACTGTGAGAGGCCACCGTTCCTGCGAGATCAAGTGTCACTCAAGC 780
Qy 781 ACCGCTTTGCCAGAGTTGACAGAGCTTTGGGAGCGCCGGAGAGCTGTGGGTGGCC 840
Db 781 ACCGCTTTGCCAGAGTTGACAGAGCTTTGGGAGCGCCGGAGAGCTGTGGGTGGCC 840
Qy 841 GCTTTCTGAGAGAGGGCCCGAGAGAAACAGTGCCTATGAGCAGTGTGTCTGGCTTG 900
Db 841 GCTTTCTGAGAGAGGGCCCGAGAGAAACAGTGCCTATGAGCAGTGTGTCTGGCTTG 900
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAAGAGTCAAGTCCAGAGTCAATATCTGCACTC 960
Db 901 GAAAGAAATGCTGAGAGAGGCTCAAGAGTCAAGTCCAGAGTCAATATCTGCACTC 960
Qy 961 CTGGCTCTGAGATTTAGAGCGGCTTCCAAATAGAGGGGTCTCTGACTACACCGCTGT 1020
Db 961 CTGGCTCTGAGATTTAGAGCGGCTTCCAAATAGAGGGGTCTCTGACTACACCGCTGT 1020
Qy 1021 GCCCAGGGGTGATCTGAGCTGTGTTTAAACAGAGAGTATCTGAGTCAAGAGCTC 1080
Db 1021 GCCCAGGGGTGATCTGAGCTGTGTTTAAACAGAGAGTATCTGAGTCAAGAGCTC 1080
Qy 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGTAATCTGCGCTCAAGCTAACTTCGGA 1140
Db 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGTAATCTGCGCTCAAGCTAACTTCGGA 1140
Qy 1141 GCGAGGCGAGCTTAAATGGGGAGTGAATGAGGCTCTTCCCTGCTGAGTGAACAGC 1200
Db 1141 GCGAGGCGAGCTTAAATGGGGAGTGAATGAGGCTCTTCCCTGCTGAGTGAACAGC 1200
Qy 1201 AGTCTCGGGCTGCTGAGCAGTCAAGTGAATCTCTGCTGAGTGTGTAATCTCA 1260
Db 1201 AGTCTCGGGCTGCTGAGCAGTCAAGTGAATCTCTGCTGAGTGTGTAATCTCA 1260
Qy 1261 GCGCTGTTTTTGGCTCTCTTTTCTGTCAACAGCGTGGCTTCTTGTGCAATGGA 1320
Db 1261 GCGCTGTTTTTGGCTCTCTTTTCTGTCAACAGCGTGGCTTCTTGTGCAATGGA 1320
Qy 1321 AGGAGCACAAGAGGGAGAACCAAGGGGGTGTGACTCCGCCAGAGAGAGTGGCCAG 1380
Db 1321 AGGAGCACAAGAGGGAGAACCAAGGGGGTGTGACTCCGCCAGAGAGAGTGGCCAG 1380
Qy 1381 ACTGAGGCTTGAAGGCTGATCTTGAAGATGTGAAGACCAAGAGGATCTGAAGG 1440
Db 1381 ACTGAGGCTTGAAGGCTGATCTTGAAGATGTGAAGACCAAGAGGATCTGAAGG 1440
Qy 1441 GAGAGCGGTAACTGTCTGTCTCTGCTCATATATGCACTTCTTTAACTGCAAGAAAT 1500
Db 1441 GAGAGCGGTAACTGTCTGTCTCTGCTCATATATGCACTTCTTTAACTGCAAGAAAT 1500

Qy 1501 TTTTAAATAATATTTATTAAT 1522
Db 1501 TTTTAAATAATATTTATTAAT 1522

RESULT 5
ADK41803
ID ADK41803 standard; DNA, 1522 BP.
XX
AC ADK41803;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human MN gene sequence SegID1.
XX
KW carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
KW human; vertebrate; cytostatic; vaccine; gene therapy;
KW renal cell carcinoma; breast cancer; colorectal cancer; ds; gene.
XX
OS Homo sapiens.

Key Location/Qualifiers
FT CDS 13..1392
FT /tag= a
FT /product= "Human MN protein"

MO2004005348-A1.
XX
PD 15-JAN-2004.
XX
PD 22-FEB-2003; 2003WO-US005137.
XX
PR 23-MAY-2002; 2002US-0383068P.
XX
PR 05-DEC-2002; 2002US-0431499P.
XX
PA (FAR) BAYER CORP.
XX (VIR-) INST VIROLOGY.
XX
PI Zavada J, Pastorekova S, Pastorek J, Zavadvova Z;
XX
DR WPI; 2004-083500/08.
XX P-PSDB; ADK41804.

FT New soluble form of the carbonic anhydrase IX (CA IX) protein for
FT screening, diagnosing or prognosing diseases associated with abnormal
FT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
FT colorectal cancer.
XX
XX
PS Disclosure; SEQ ID NO 1; 159pp; English.

CC This invention relates to a novel soluble form of the carbonic anhydrase
CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.
CC The invention may be useful for the development of compounds with a
CC cyostatic activity or a vaccine whilst the disclosed sequences may be
CC used for gene therapy. The protein and method are useful for screening,
CC diagnosing or prognosing diseases associated with abnormal expression of
CC carbonic anhydrase IX protein, such as precancerous and cancerous
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.
CC The monoclonal antibody may also be used for treating or preventing
CC precancerous and cancerous diseases. The present sequence is that of the
CC gene which encodes the human MN protein of the invention.
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 12; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAAGCGCATGCTCCCTGTGGCCAGGCCCTGCTCTGTGATCCCGGCC 60
Db 1 ACAGTCAAGCGCATGCTCCCTGTGGCCAGGCCCTGCTCTGTGATCCCGGCC 60

PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236039P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 3116; 44bp; English.

XX The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AB161664 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytotoxic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell, cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms tumor

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 6; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGTCAGCCGATGCTCCCTGTGCCAGCCCTGGCTCCCTGTGTGATCCGGCC 60
DB 31 ACAAGTCAGCCGATGCTCCCTGTGCCAGCCCTGGCTCCCTGTGTGATCCGGCC 90
QY 61 CCTGTCCAGGCTCACTGTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 120
DB 91 CCTGTCCAGGCTCACTGTGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 150
QY 121 CCCGAGAGTTGCCCGGATGAGAGATTTCCCTTTGGAGAGGCTTTTGGGGA 180
DB 151 CCCGAGAGTTGCCCGGATGAGAGATTTCCCTTTGGAGAGGCTTTTGGGGA 210
QY 181 GATGACCACTGGGCGAGAGAGATTTGCCCAAGAGAGATTTCAACGAGAGAGGAT 240

DB 211 GATGACCACTGGGCGAGAGAGATTTGCCCAAGAGAGATTTCAACGAGAGAGGAT 270
QY 241 CCACCCGAGAGAGAGATTTCACTGTGAGAGAGATTTCACTGTGAGAGAGATTTACT 300
DB 271 CCACCCGAGAGAGAGATTTCACTGTGAGAGAGATTTCACTGTGAGAGAGATTTACT 330
QY 301 GAAGTTAAGCTTAATCAAGAGAGAGGCTTCCCTGAAGTTAGAGATTTACTTCTGT 360
DB 331 GAAGTTAAGCTTAATCAAGAGAGAGGCTTCCCTGAAGTTAGAGATTTACTTCTGT 390
QY 361 GAGGCTCTGGAGATTCCTCAAGAACCCCAAGATTAATGCCCAGGAGCAAGAGAGGAT 420
DB 391 GAGGCTCTGGAGATTCCTCAAGAACCCCAAGATTAATGCCCAGGAGCAAGAGAGGAT 450
QY 421 GACCAAGTCAATTGGCGCTATGAGGCGACCCGCGCTGAGCCCGGCTTCCCAAGCTGC 480
DB 451 GACCAAGTCAATTGGCGCTATGAGGCGACCCGCGCTGAGCCCGGCTTCCCAAGCTGC 510
QY 481 GCGGCGCGCTTCCAGTCCCGGCTGATATCCGCGCCCAAGCTTCCGCTTCCCGGCGC 540
DB 511 GCGGCGCGCTTCCAGTCCCGGCTGATATCCGCGCCCAAGCTTCCGCTTCCCGGCGC 570
QY 541 CTGCGCGCGCTTCCAGTCCCGGCTTCCAGCTCCCGCGCTCCCAAGCTGCGCTGCGC 600
DB 571 CTGCGCGCGCTTCCAGTCCCGGCTTCCAGCTCCCGCGCTCCCAAGCTGCGCTGCGC 630
QY 601 AACAAATGCGCAAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGCTTGGGTC 660
DB 631 AACAAATGCGCAAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGCTTGGGTC 690
QY 661 GCGCGGAGATTCGCGGCTTCCAGTGTGATCTGCACTGAGGCGGCTGCAAGTCTCGGCGC 720
DB 691 GCGCGGAGATTCGCGGCTTCCAGTGTGATCTGCACTGAGGCGGCTGCAAGTCTCGGCGC 750
QY 721 TCGAGGACACTGTGAAAGGCGACCGTTTCCCTGCGGAGATTCAGTGTTCACCTGAGC 780
DB 751 TCGAGGACACTGTGAAAGGCGACCGTTTCCCTGCGGAGATTCAGTGTTCACCTGAGC 810
QY 781 ACCGCTTTGCGCAAGTGTGCAAGGCGCTTGGGCGCGCGGAGGCTTGGGTC 840
DB 811 ACCGCTTTGCGCAAGTGTGCAAGGCGCTTGGGCGCGCGGAGGCTTGGGTC 870
QY 841 GCGTTTGTGAGAGAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 871 GCGTTTGTGAGAGAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 901 GAAAGAAATCGTGAAGAGGCTCAGAGACTCAGAGTCCAGAGACTGACATATTCGACTC 960
DB 931 GAAAGAAATCGTGAAGAGGCTCAGAGACTCAGAGTCCAGAGACTGACATATTCGACTC 990
QY 961 CTGCGCTGTGACTTCAAGCGGCTTCAATATATGAGGAGTCTTGTACTACACCGCTGT 1020
DB 991 CTGCGCTGTGACTTCAAGCGGCTTCAATATATGAGGAGTCTTGTACTACACCGCTGT 1050
QY 1021 GCCAGAGGTGATCTGAGTGTGATTAACAGACAGAGATGAGTGAAGAGCTC 1080
DB 1051 GCCAGAGGTGATCTGAGTGTGATTAACAGACAGAGATGAGTGAAGAGCTC 1110
QY 1081 CACACCTCTGTGACACCTGTGAGGAGCTTGTGACTTCCGCTACAGCTGACTTCCGA 1140
DB 1111 CACACCTCTGTGACACCTGTGAGGAGCTTGTGACTTCCGCTACAGCTGACTTCCGA 1170
QY 1141 GCGAGCGAGCTTGAATGAGGCGAGATTAAGGCTTCTTCCCTGTGAGTGAAGC 1200
DB 1171 GCGAGCGAGCTTGAATGAGGCGAGATTAAGGCTTCTTCCCTGTGAGTGAAGC 1230
QY 1201 AGTCTGCGGCTGTGAGCGACAGTCAAGTGAATTCGCGCTGAGTGGAGATCTCTA 1260
DB 1231 AGTCTGCGGCTGTGAGCGACAGTCAAGTGAATTCGCGCTGAGTGGAGATCTCTA 1290
QY 1261 GCGCTGATTTTGGCTCTTTTGTGTGCTGACACAGCGTCCGCTTGTGTGAGATGAGA 1320
DB 1291 GCGCTGATTTTGGCTCTTTTGTGTGCTGACACAGCGTCCGCTTGTGTGAGATGAGA 1350

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OY 1321 AGGACACAGAGGGGAAACAAAGGGGGGTGTGAGCTACCGCCAGAGAGTGGCCGAG 1380
    |||||
DB 1351 AGGACACAGAGGGGAAACAAAGGGGGGTGTGAGCTACCGCCAGAGAGTGGCCGAG 1410
OY 1381 ACTGAGCCTTAGAGGCTGTGATCTTGGAGATGTGAGAGCCAGAGGCATCTGAGGG 1440
    |||||
DB 1411 ACTGAGCCTTAGAGGCTGTGATCTTGGAGATGTGAGAGCCAGAGGCATCTGAGGG 1470
OY 1441 GAGAGCGGTAACTGTCTGTCTCTGCTCATTTATGCCCTTCTTTAACTGCCAAGAAAT 1500
    |||||
DB 1471 GAGAGCGGTAACTGTCTGTCTCTGCTCATTTATGCCCTTCTTTAACTGCCAAGAAAT 1530
OY 1501 TTTTAAATTAATTAATTTATTAAT 1522
    |||||
DB 1531 TTTTAAATTAATTAATTTATTAAT 1552

RESULT 7
ABL62179
ID ABL62179 standard; DNA; 1552 BP.
XX
AC ABL62179;
XX
DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:516.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
    stomach; lung; prostate; pancreas; carcinoma; antitumour; carcinos;
    cytotoxic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
    gene; db.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
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PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX MPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 516; 44dp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
XX neoplastic agent. The method involves exposing cells to a chemical agent
XX to be tested for anti-neoplastic activity, determining a change in (I)
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL6164
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening an
XX anti-neoplastic agent, and can be used for producing a product which is
XX the data collected with respect to the anti-neoplastic agent as a result
XX of M1, and the data is sufficient to convey the chemical structure and/or
XX properties of the agent. M1 can be used in the treatment of cancer such
XX as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
XX prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
XX cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
XX cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
XX tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ACAGTCAGCGGATGATGCTCCCTGTCGCCAGCCCTGCTCCTGTTGATCCCGGCC 60
    |||||
DB 31 ACAGTCAGCGGATGATGCTCCCTGTCGCCAGCCCTGCTCCTGTTGATCCCGGCC 90
OY 61 CCTGCTCCAGGCTCTCACTGTGCACTGTCTGTCTCACTGCTGTTTGTATGCTGTCAT 120
    |||||
DB 91 CCTGCTCCAGGCTCTCACTGTGCACTGTCTGTCTCACTGCTGTTTGTATGCTGTCAT 150
OY 121 CCCGAGAGTTGCTCCCGGATGCAAGAGATTTCCCTTTGGAGAGAGCTCTTTTGGGAA 180
    |||||
DB 151 CCCGAGAGTTGCTCCCGGATGCAAGAGATTTCCCTTTGGAGAGAGCTCTTTTGGGAA 210
OY 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGAT 240
    |||||
DB 211 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGAT 270
OY 241 CCACCCGAGAGAGAGATCTTACCTGAGAGAGATCTTACCTGAGAGAGAGATCTTACCT 300
    |||||
DB 271 CCACCCGAGAGAGAGATCTTACCTGAGAGAGATCTTACCTGAGAGAGAGATCTTACCT 330
OY 301 GAAGTTAAGCTTAATCAAGAAGAGGCTCCCTGAATGTAGAGATCTTACTTACTT 360
    |||||
DB 331 GAAGTTAAGCTTAATCAAGAAGAGGCTCCCTGAATGTAGAGATCTTACTTACTT 390
OY 361 GAGGCTCTGAGATCTTCAAGAACCCAGAAATTAATGCCACAGGAGCAAGAGAGGAT 420
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Db 391 GAGGCTCTGGAGATCTCAAGAACCCAGAAATAAGCCACAGGAAACAAGAGAGGAGAT 450
Qy 421 GACCAAGATCATTTGGGCTATGAGAGGGAACCCGCTGGGCTCCGGGATGCCAGGCTGC 480
Db 451 GACCAAGATCATTTGGGCTATGAGAGGGAACCCGCTGGGCTCCGGGATGCCAGGCTGC 510
Qy 481 GCGGGGCGCTTCCAGTCCCGGATGATATCCGCCCCAGTCCGCGCTTCTGCCCCGCC 540
Db 511 GCGGGGCGCTTCCAGTCCCGGATGATATCCGCCCCAGTCCGCGCTTCTGCCCCGCC 570
Qy 541 CTGCGCCCCCTGGAACTCTGAGGCTTCCAGCTCCGCGCTCCAGAACTGCGGCTGGCG 600
Db 571 CTGCGCCCCCTGGAACTCTGAGGCTTCCAGCTCCGCGCTCCAGAACTGCGGCTGGCG 630
Qy 601 AACCAATGCCACAGTGTGCACTGACCTGCTCTGAGGCTAGAGATGAGCTGTGAGTCC 660
Db 631 AACCAATGCCACAGTGTGCACTGACCTGCTCTGAGGCTAGAGATGAGCTGTGAGTCC 690
Qy 661 GGGCGGAGATACCGGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 720
Db 691 GGGCGGAGATACCGGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 750
Qy 721 TCGAGACACATGTTGAGAGGCAACGCTTCCGCGGAGATCCAGGTTGCTTCACTGAGC 780
Db 751 TCGAGACACATGTTGAGAGGCAACGCTTCCGCGGAGATCCAGGTTGCTTCACTGAGC 810
Qy 781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGGGGCGCCGCGAGAGCTGAGCTGTGGCC 840
Db 811 ACCGCTTTTGCAGAGTTGACAGAGGCTTGGGGCGCCGCGAGAGCTGAGCTGTGGCC 870
Qy 841 GCTTTTGGAGAGAGGCCCCGAGAGAAACAAGTCTTAAGAGAGTGTGCTGTGCTGG 900
Db 871 GCTTTTGGAGAGAGGCCCCGAGAGAAACAAGTCTTAAGAGAGTGTGCTGTGCTGG 930
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGTGAATCTGCACTC 960
Db 931 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGTGAATCTGCACTC 990
Qy 961 CTGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGCTCTCTGACTACACCGCTGT 1020
Db 991 CTGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGCTCTCTGACTACACCGCTGT 1050
Qy 1021 GCGCAGGGGTCATCTGAGCTGAGTGTAAACAGACAGTATCTGAGTGAAGAGCTC 1080
Db 1051 GCGCAGGGGTCATCTGAGCTGAGTGTAAACAGACAGTATCTGAGTGAAGAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGAGGAGCTGAGTACTCTGAGCTACAGCTGAATCTCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGAGGAGCTGAGTACTCTGAGCTACAGCTGAATCTCCGA 1170
Qy 1141 GCGAGCGAGCTTTGATATGAGGCGAGTGAAGGCTCTCTTCTGCTGAGTGAAGCAGC 1200
Db 1171 GCGAGCGAGCTTTGATATGAGGCGAGTGAAGGCTCTCTTCTGCTGAGTGAAGCAGC 1230
Qy 1201 AGTCTCTGAGGCTGAGGCACTGAGCTGAATTCCTGCTGAGGCTGAGTGAATTCCTGA 1260
Db 1231 AGTCTCTGAGGCTGAGGCACTGAGCTGAATTCCTGCTGAGGCTGAGTGAATTCCTGA 1290
Qy 1261 GCGCTGTGTTTGGCTCTCTTGTGCTGACACAGGTCGAGCTCTCTTGTGAGATGAGA 1320
Db 1291 GCGCTGTGTTTGGCTCTCTTGTGCTGACACAGGTCGAGCTCTCTTGTGAGATGAGA 1350
Qy 1321 AGGCGACACAGAGAGGAGAAACAAGGGGCTGAGACTACCGCCAGAGAGGTAGCCAG 1380
Db 1351 AGGCGACACAGAGAGGAGAAACAAGGGGCTGAGACTACCGCCAGAGAGGTAGCCAG 1410
Qy 1381 ACTGAGGCTTAGAGGCTGAGTCTTGGAGAAATGAGAGGCGAGGAGGAGGACTGAGAGG 1440
Db 1411 ACTGAGGCTTAGAGGCTGAGTCTTGGAGAAATGAGAGGCGAGGAGGAGGACTGAGAGG 1470
Qy 1441 GGAGCGGTAAGTCTGTCTGTCTGCTCATATGACACTTCTTTTAACTGCGCAAGAAAT 1500

Db 1471 GGAGCGGTAAGTCTGTCTGTCTGCTCATATGACACTTCTTTAACTGCGCAAGAAAT 1530
Qy 1501 TTTTAAATTAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAATTAAT 1552
RESULT 8
ABL65416
ID ABL65416 strand; DNA, 1552 BP.
XX
AC ABL65416;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:3753.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231133P.
PR 18-SEP-2000; 2000US-0231617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234502P.
PR 22-SEP-2000; 2000US-0234567P.
PR 22-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235712P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 28-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237117P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S,
Soppet DR, Weaver Z;

WPI, 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 3753; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABU61664 to ABU70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1522;	DB 6;	Length 1552;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1522;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	ACAGTCAGCCGATGGCTCCCCGTATCCCGAGCCCTGGCTCCCTCTGTTGATCCCGGCC	60
Db	31	ACAGTCAGCCGATGGCTCCCCGTATCCCGAGCCCTGGCTCCCTCTGTTGATCCCGGCC	90
QY	61	CCTGCTCAAGSCCTCACTGTGCACTGTGTGTCACTGTGTCTTGATGCTGTCCAT	120
Db	91	CCTGCTCAAGSCCTCACTGTGCACTGTGTGTCACTGTGTCTTGATGCTGTCCAT	150
QY	121	CCCCAGAGGTTGCCCCGGATGACAGAGGATTCGCCCTTGAGGAGAGGCTCTTCGGGGAA	180
Db	151	CCCCAGAGGTTGCCCCGGATGACAGAGGATTCGCCCTTGAGGAGAGGCTCTTCGGGGAA	210
QY	181	GATGACCCACTGGGCGAGAGGATCTGCCACATGGAAGAGATTCACTGAGAGAGAT	240
Db	211	GATGACCCACTGGGCGAGAGGATCTGCCACATGGAAGAGATTCACTGAGAGAGAT	270
QY	241	CCACCCGAGAGAGGATCTACTGTGAGAGAGGATCTACCTGGAAGAGAGATCTACCT	300
Db	271	CCACCCGAGAGAGGATCTACTGTGAGAGAGGATCTACCTGGAAGAGAGATCTACCT	330
QY	301	GAAATTAAAGCTTAAATCAGAAAGAGGGCTCCCTGAAGTTAGAGATCTACTACTGT	360
Db	331	GAAATTAAAGCTTAAATCAGAAAGAGGGCTCCCTGAAGTTAGAGATCTACTACTGT	390
QY	361	GAGGCTCCGTGAGATCTCAAGAACCCCAAGATTATGCCCAAGGCAAAAGAGGGGAT	420
Db	391	GAGGCTCCGTGAGATCTCAAGAACCCCAAGATTATGCCCAAGGCAAAAGAGGGGAT	450
QY	421	GACCAAGATCAATTGGCGCTATGAGAGCGACCCGCTGGCCCGGGTGTCCTCCAGCGCTG	480
Db	451	GACCAAGATCAATTGGCGCTATGAGAGCGACCCGCTGGCCCGGGTGTCCTCCAGCGCTG	510
QY	481	GCGGCGCGCTTCAAGTCCCGGTGATATTCGCGCCCAAGTGGCGCGCTTCTGCGCGGC	540
Db	511	GCGGCGCGCTTCAAGTCCCGGTGATATTCGCGCCCAAGTGGCGCGCTTCTGCGCGGC	570

QY	541	CTGGGCCCCCTGGAACCTCTG6GGCTTCAGATCCCGGCGCTCCAGAACTGCGCTGCGC	600
Db	571	CTGGGCCCCCTGGAACCTCTG6GGCTTCAGATCCCGGCGCTCCAGAACTGCGCTGCGC	630
QY	601	AACAATGCGCACAAGTGTGCAA CTGACCCCTGCTCTTGGGCTTAAGATGAGTCTTGGGTCCC	660
Db	631	AACAATGCGCACAAGTGTGCAA CTGACCCCTGCTCTTGGGCTTAAGATGAGTCTTGGGTCCC	690
QY	661	GGGGGGGAGTACCGGGGCTTCGACCTGCATCTGTGACTGGGGGGGGTGGACGGTCCGGGGC	720
Db	691	GGGGGGGAGTACCGGGGCTTCGACCTGCATCTGTGACTGGGGGGGGTGGACGGTCCGGGGC	750
QY	721	TGGAGGACACTGTGTGAAGGCGACCGTTCCTCGCCGAGATCCAGTGTGTTCACTGAGC	780
Db	751	TGGAGGACACTGTGTGAAGGCGACCGTTCCTCGCCGAGATCCAGTGTGTTCACTGAGC	810
QY	781	ACCGCCTTTGCTCAGAGTTGACGAGGCTTTGGGGCGCCCGGGAGGCTGGCCCTGTGTGGCC	840
Db	811	ACCGCCTTTGCTCAGAGTTGACGAGGCTTTGGGGCGCCCGGGAGGCTGGCCCTGTGTGGCC	870
QY	841	GCCTTTCTGAGGAGGGGCGCGGAGAAACAAGTGCCTATGAGCAGTTCGTCTCGCTTG	900
Db	871	GCCTTTCTGAGGAGGGGCGCGGAGAAACAAGTGCCTATGAGCAGTTCGTCTCGCTTG	930
QY	901	GAGAAATTCGCTGAGGAAGGCTCAGAGCTTCAGGCTCCAGGACTGGAATATCTGCACTC	960
Db	931	GAGAAATTCGCTGAGGAAGGCTCAGAGCTTCAGGCTCCAGGACTGGAATATCTGCACTC	990
QY	961	CTGCCCTCTCTGACTTCAGCCGCTACTTCCTCAATATGAGGGGTCTTCTGACTACACCGCCTGT	1020
Db	991	CTGCCCTCTCTGACTTCAGCCGCTACTTCCTCAATATGAGGGGTCTTCTGACTACACCGCCTGT	1050
QY	1021	GCCAGGGGTGCATCTGGACTGTGCTTTAAACAAGACAGTATGCTGAGTGCATACAGCTC	1080
Db	1051	GCCAGGGGTGCATCTGGACTGTGCTTTAAACAAGACAGTATGCTGAGTGCATACAGCTC	1110
QY	1081	CACAACCTCTCTGACAACCTGTGTGGAGACTGTGTGACTTCGCGCTACAGCTGAACCTTCGA	1140
Db	1111	CACAACCTCTCTGACAACCTGTGTGGAGACTGTGTGACTTCGCGCTACAGCTGAACCTTCGA	1170
QY	1141	GCGACGCAAGCTTTGAATGGGCGAGTATTAAGGCTCTTCCTCGCTGAGTGTGAACAGC	1200
Db	1171	GCGACGCAAGCTTTGAATGGGCGAGTATTAAGGCTCTTCCTCGCTGAGTGTGAACAGC	1230
QY	1201	AGTCTCTGGGGCTGCTGAGCGCAGTCCAGCTGAATTCCTGCGCTGGGCTGCTGTGAATCTCTA	1260
Db	1231	AGTCTCTGGGGCTGCTGAGCGCAGTCCAGCTGAATTCCTGCGCTGGGCTGCTGTGAATCTCTA	1290
QY	1261	GCCTGTGTTTTGCGCTCTCTTTTGTGCTGTCAACAGCGTCCGGTTCCTTGTGCAATGAGA	1320
Db	1291	GCCTGTGTTTTGCGCTCTCTTTTGTGCTGTCAACAGCGTCCGGTTCCTTGTGCAATGAGA	1350
QY	1321	AGGCAAGCACAAGAGGGGAAACCAAGGGGGGTGTAGTACACCGCCAGCAGAGTGTGCCGAG	1380
Db	1351	AGGCAAGCACAAGAGGGGAAACCAAGGGGGGTGTAGTACACCGCCAGCAGAGTGTGCCGAG	1410
QY	1381	ACTGAGGCTGTGAGGCTGTGATCTTGTGAGAAATGTAGAGACAGGCGCAGGCGATCTGAGGG	1440
Db	1411	ACTGAGGCTGTGAGGCTGTGATCTTGTGAGAAATGTAGAGACAGGCGCAGGCGATCTGAGGG	1470
QY	1441	GGAGCCGGTAACTGTCTCTGTCTGTCTCATTAATGCACTTCCTTTTAACTGCGCAAGAAAT	1500
Db	1471	GGAGCCGGTAACTGTCTCTGTCTGTCTCATTAATGCACTTCCTTTTAACTGCGCAAGAAAT	1530
QY	1501	TTTTTAAATTAATATTTATATAT 1522	
Db	1531	TTTTTAAATTAATATTTATATAT 1552	

RESULT	9
ABL68346	
ID	ABL68346 standard; DNA; 1552 BP.
XX	

AC ABL68346;
XX
DT 15-MAY-2002 (first entry)
XX
DE Kidney cancer related gene sequence SEQ ID NO:6683.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN MO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001MO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrisan S;
PI Sopet DR, Weaver Z;
XX
DR WPI: 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX

PS Claim 1; SEQ ID NO 6683; 44bp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in (I)
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophagal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCACGCCGATGGCTCCCTGTGCCCAAGCCCTGGTCCCTCTGTGATCCCGGCC 60
DB 31 ACAGTCACGCCGATGGCTCCCTGTGCCCAAGCCCTGGTCCCTCTGTGATCCCGGCC 90
QY 61 CCTGTCACAGCCCTCACTGTGTGCACTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 120
DB 91 CCTGTCACAGCCCTCACTGTGTGCACTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 150
QY 121 CCCAGAGGTTGCCCGGATCAGAGAGATTTCCCTTGGAGAGAGGCTCTTGGAGAA 180
DB 151 CCCAGAGGTTGCCCGGATCAGAGAGATTTCCCTTGGAGAGAGGCTCTTGGAGAA 210
QY 181 GATGACCCATCGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCATCGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTCTCTGAGAGAGAGATCTACTCTGAGAGAGAGATTTACT 300
DB 271 CCACCCGAGAGAGAGATCTCTCTGAGAGAGAGATCTACTCTGAGAGAGAGATTTACT 330
QY 301 GAAGTTAAGCTTAATCAAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 390
QY 361 GAGGCTCTGAGAGATCTCTCAAGAAACCCAGATTAATGCCACAGAGACAAAGAGGAT 420
DB 391 GAGGCTCTGAGAGATCTCTCAAGAAACCCAGATTAATGCCACAGAGACAAAGAGGAT 450
QY 421 GACCAAGATCATTTGGCGCTATGAGAGGAGACCCGCGCTGGCGCGGGGTCTCCCAAGCTTC 480
DB 451 GACCAAGATCATTTGGCGCTATGAGAGGAGACCCGCGCTGGCGCGGGGTCTCCCAAGCTTC 510
QY 481 GCGGCGCGCTTCAAGTCCCGGATGATATCGCCCAAGCTCGCGGCTTCTGCGCGGCC 540
DB 511 GCGGCGCGCTTCAAGTCCCGGATGATATCGCCCAAGCTCGCGGCTTCTGCGCGGCC 570
QY 541 CTGCGCGCCCTTGAACTCTGAGGCTTCAAGTCTCCGCGCTCCCAAGATCTGCGCTGGGC 600
DB 571 CTGCGCGCCCTTGAACTCTGAGGCTTCAAGTCTCCGCGCTCCCAAGATCTGCGCTGGGC 630
QY 601 AACATGGCCACAGTGTGCACTGACCTGCTCTGAGGCTCTGAGAGATCTGAGGCTTCC 660
DB 631 AACATGGCCACAGTGTGCACTGACCTGCTCTGAGGCTCTGAGAGATCTGAGGCTTCC 690
QY 661 GGGGAGAGATACCGGAGCTGTGACAGCTCATCTGCACTGGGAGGCTGCAAGTCTCCGGCC 720
DB 691 GGGGAGAGATACCGGAGCTGTGACAGCTCATCTGCACTGGGAGGCTGCAAGTCTCCGGCC 750

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QY 721 TCGAGACACATGTGAGAGCCACCGTTTCCCTGCGGAGATCCAGTGGTTCACTCAGC 780
DB 751 TCGAGACACATGTGAGAGCCACCGTTTCCCTGCGGAGATCCAGTGGTTCACTCAGC 810
QY 781 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGCGCCCGGAGAGGCTGGCCGTGGGCC 840
DB 811 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGCGCCCGGAGAGGCTGGCCGTGGGCC 870
QY 841 GCTTTTCTGAGAGAGAGGCCCCGAGAGAAACAGTGCCTTAGAGAGTGGTCTGTCCCTGG 900
DB 871 GCTTTTCTGAGAGAGAGGCCCCGAGAGAAACAGTGCCTTAGAGAGTGGTCTGTCCCTGG 930
QY 901 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGACTGAGCAATATCGACATC 960
DB 931 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGACTGAGCAATATCGACATC 990
QY 961 CTGCTCTGACTTACGCGCTACTTCCAAATATGAGGGGTCTTCTGACTACCGCCCTGT 1020
DB 991 CTGCTCTGACTTACGCGCTACTTCCAAATATGAGGGGTCTTCTGACTACCGCCCTGT 1050
QY 1021 GCGGAGGCTGCTGACTGAGTGTGTTAACAGAGAGTATGCTGAGTCTAGACAGCTTC 1080
DB 1051 GCGGAGGCTGCTGACTGAGTGTGTTAACAGAGAGTATGCTGAGTCTAGACAGCTTC 1110
QY 1081 CACACCTCTGAGACACCGCTGAGGAGACCTGAGTACTCTCGGCTACAGCTGAATCTCCGA 1140
DB 1111 CACACCTCTGAGACACCGCTGAGGAGACCTGAGTACTCTCGGCTACAGCTGAATCTCCGA 1170
QY 1141 GCGAGCGACCTTTGATGATGGGCGAGTATGAGGCTCTCTCTGCTGAGTGAACAGC 1200
DB 1171 GCGAGCGACCTTTGATGATGGGCGAGTATGAGGCTCTCTCTGCTGAGTGAACAGC 1230
QY 1201 AGTCTCTGGGCTGCTGAGACAGTCCAGCTGAATCTCTGCTGCTGCTGCTGATCTCTA 1260
DB 1231 AGTCTCTGGGCTGCTGAGACAGTCCAGCTGAATCTCTGCTGCTGCTGCTGATCTCTA 1290
QY 1261 GGCCTGGTTTTGGGCTCTCTTTTGGTGCACAGAGGCTGGCTCTGCTGAGATGAGA 1320
DB 1291 GGCCTGGTTTTGGGCTCTCTTTTGGTGCACAGAGGCTGGCTCTGCTGAGATGAGA 1350
QY 1321 AGCGACACAGAGAGGAGAACAAAGGGGTGTGAGTACCGCCAGCAGAGTGAAGCCGAG 1380
DB 1351 AGCGACACAGAGAGGAGAACAAAGGGGTGTGAGTACCGCCAGCAGAGTGAAGCCGAG 1410
QY 1381 ACTGAGCTTGAAGGCTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGGATCTGAGG 1440
DB 1411 ACTGAGCTTGAAGGCTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGGATCTGAGG 1470
QY 1441 GGAGCGGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1471 GGAGCGGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
QY 1501 TTTTAAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAAT 1552

```

RESULT 10
ABX76385
ID ABX76385 standard; DNA; 1552 BP.
XX
AC ABX76385;

DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #249.
XX

KM Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hyperresponsivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

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XX OS Unidentified.
XX PN WO200286443-A2.
XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US012476.
XX 18-APR-2001; 2001US-0284770P.
XX 10-MAY-2001; 2001US-0290492P.
XX 09-NOV-2001; 2001US-0339245P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI: 2003-093161/08.
XX P-PSDB; ABUS6656.
XX DR
XX DR
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer.
XX PS Claim 22; Page 379-380; 453pp; English.
XX
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX CC for diagnostic purposes and as targets for screening for therapeutic
XX CC compounds that modulate lung cancer, such as antibodies. Sequences
XX CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
XX CC invention
XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGCTCCTCTGTGATCCCGGCC 60
DB 31 ACAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGCTCCTCTGTGATCCCGGCC 90
QY 61 CCTGCTCAGGCTCAGCTGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCTGCTCAGGCTCAGCTGTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCAGAGGTTGCCCGAGTGCAGAGATTCCTTGGGAGAGGCTCTTCTGAGGAA 180
DB 151 CCCAGAGGTTGCCCGAGTGCAGAGATTCCTTGGGAGAGGCTCTTCTGAGGAA 210
QY 181 GATGACCCACTGGGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT 300

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Db	271	CCACC	CGGAGAGGAGTCTACTGGAGGAGGATCTACTGAGAGGAGTCTA	CCT	330
QY	301	GAA	GTAAACCTTAATCATGAAGAAAGAGGCTCCCTGAAGTTAAGATCTA	CTACTGT	360
Db	331	GAA	GTAAACCTTAATCATGAAGAAAGAGGCTCCCTGAAGTTAAGATCTA	CTACTGT	390
QY	361	GAG	GCTCCTGAGATCTCAAGAACCCAGAAATATATGCCACAGGGGCA	AAAGAGGAGAT	420
Db	391	GAG	GCTCCTGAGATCTCAAGAACCCAGAAATATATGCCACAGGGGCA	AAAGAGGAGAT	450
QY	421	GAC	CAGATCATTTGGCGCTATGAGGCGACCCGCTGGCCCGGAGTCCC	AGCCTGC	480
Db	451	GAC	CAGATCATTTGGCGCTATGAGGCGACCCGCTGGCCCGGAGTCCC	AGCCTGC	510
QY	481	GCG	GGGCGCGCTTCACAGTCCCCGGAGATATCCCGCCCAAGTGGCCGC	CTTCTGCGCGGC	540
Db	511	GCG	GGGCGCGCTTCACAGTCCCCGGAGATATCCCGCCCAAGTGGCCGC	CTTCTGCGCGGC	570
QY	541	CTG	CGCCCCCTGGAATCTCTGGGCTTTCAGACTCCGCGCTCCAGAACT	GCCTGCGC	600
Db	571	CTG	CGCCCCCTGGAATCTCTGGGCTTTCAGACTCCGCGCTCCAGAACT	GCCTGCGC	630
QY	601	AAC	CAATGGCCACAGTGTGAACTGAACCTTGGCTCTCGGCTAGAAAT	TGCTCGGATCCC	660
Db	631	AAC	CAATGGCCACAGTGTGAACTGAACCTTGGCTCTCGGCTAGAAAT	TGCTCGGATCCC	690
QY	661	GCG	CGGAGATACCGGAGCTCTGAGCTGCATCTGCACTGGGGGGCTCA	GAGTCGTCCGGGC	720
Db	691	GCG	CGGAGATACCGGAGCTCTGAGCTGCATCTGCACTGGGGGGCTCA	GAGTCGTCCGGGC	750
QY	721	TGG	AGCACACCTGTGGAAGGCCACCGTTTCCCTGCCGAGATCAAGT	GTTCACCTCAGC	780
Db	751	TGG	AGCACACCTGTGGAAGGCCACCGTTTCCCTGCCGAGATCAAGT	GTTCACCTCAGC	810
QY	781	ACC	GCCTTTGGCCAGATTGACGAGGGCTTGGGGGCGCCGGGAGGCG	CTGGCCGTTGGGC	840
Db	811	ACC	GCCTTTGGCCAGATTGACGAGGGCTTGGGGGCGCCGGGAGGCG	CTGGCCGTTGGGC	870
QY	841	GCT	TTCTGAGAGAGGGCCCGAAGAAAACAGTGCTATGACAGATTG	CTGTCTCGCTTG	900
Db	871	GCT	TTCTGAGAGAGGGCCCGAAGAAAACAGTGCTATGACAGATTG	CTGTCTCGCTTG	930
QY	901	GAA	GAAATCGCTGAGAGAGGCTCAAGAACTCAGGTCCAGACTGGA	CAATCTGCATC	960
Db	931	GAA	GAAATCGCTGAGAGAGGCTCAAGAACTCAGGTCCAGACTGGA	CAATCTGCATC	990
QY	961	CTG	CCCTCTGACTTCAAGCGCTACTTCCAAATATGAGGGGCTCTG	CACTACCGCCCTGT	1020
Db	991	CTG	CCCTCTGACTTCAAGCGCTACTTCCAAATATGAGGGGCTCTG	CACTACCGCCCTGT	1050
QY	1021	GCC	CAGGGTGTATCTGCACTGTGTTTAAACGACAGTATGTGATG	ATGCTTAAAGCACTC	1080
Db	1051	GCC	CAGGGTGTATCTGCACTGTGTTTAAACGACAGTATGTGATG	ATGCTTAAAGCACTC	1110
QY	1081	CAC	ACCTCTCTGACACCTCTGGGGGACCTGTGTGACTCTCGGCT	CACAGTGAATTTCCGA	1140
Db	1111	CAC	ACCTCTCTGACACCTCTGGGGGACCTGTGTGACTCTCGGCT	CACAGTGAATTTCCGA	1170
QY	1141	GCG	ACGACTTGAATATGAGGCGAGTATATGAGGCTCTCTCTG	AGATGAGACAGC	1200
Db	1171	GCG	ACGACTTGAATATGAGGCGAGTATATGAGGCTCTCTCTG	AGATGAGACAGC	1230
QY	1201	AGT	CTCGGGGCGTGAAGCAGATCCAGAGTAATTCGTGCGGCTG	CGTGTGTAACATCCGA	1260
Db	1231	AGT	CTCGGGGCGTGAAGCAGATCCAGAGTAATTCGTGCGGCTG	CGTGTGTAACATCCGA	1290
QY	1261	GCC	CTGTATTTTGGCTCTTTTGTCTGTCAACAGCGTTCGCTT	CTTGTGACAGATATGAG	1320
Db	1291	GCC	CTGTATTTTGGCTCTTTTGTCTGTCAACAGCGTTCGCTT	CTTGTGACAGATATGAG	1350
QY	1321	AGG	CAGCACAGAAAGGGGAACAAAGGGGTGTAGCTACCGCC	CACAGAGGTATGCCAG	1380

[illegible]

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The gene, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX7474 represent lung cancer-associated polynucleotides of the
CC invention

XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AAGTCAGCGCGAGTGGCTCCCTGTCGCGCCGAGCCCTGCTCCCTGTTGATCCCGGAC 60
DB 31 AAGTCAGCGCGAGTGGCTCCCTGTCGCGCCGAGCCCTGCTCCCTGTTGATCCCGGAC 90
QY 61 CCGCTCCAGGCTCACTGTCGCACTGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCGCTCCAGGCTCACTGTCGCACTGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCCAGAGGTGGCCCGGATGCAAGAGATTCCTCCCTTGGAGAGAGCTTTCTGGGAA 180
DB 151 CCCCAGAGGTGGCCCGGATGCAAGAGATTCCTCCCTTGGAGAGAGCTTTCTGGGAA 210
QY 181 GATGACCCGCTGGCGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
DB 211 GATGACCCGCTGGCGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCT 300
DB 271 CCACCCGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCT 330
QY 301 GAAGTTAGCTTAATCAGAGAGAGAGCTCCCTGAAGTTAGAGATTCACCTACTGTT 360
DB 331 GAAGTTAGCTTAATCAGAGAGAGAGCTCCCTGAAGTTAGAGATTCACCTACTGTT 390
QY 361 GAGGCTCCCTGAGAGATTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 420
DB 391 GAGGCTCCCTGAGAGATTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 450
QY 421 GACAGAGATCATTTGGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
DB 451 GACAGAGATCATTTGGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 510
QY 481 GCGGCGCGCTTCCAGTCCCGGATGATTCGCGCCGAGCTGCGCTTCTGCGCGCC 540
DB 511 GCGGCGCGCTTCCAGTCCCGGATGATTCGCGCCGAGCTGCGCTTCTGCGCGCC 570
QY 541 CCGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCCAAGATCGCGCTGCGC 600
DB 571 CCGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCCAAGATCGCGCTGCGC 630
QY 601 AACCAATGGCCAGTGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 631 AACCAATGGCCAGTGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
QY 661 GGGCGGAGTACCGGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 691 GGGCGGAGTACCGGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
QY 721 TGGAGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 780
DB 751 TGGAGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 810
QY 781 ACCGCTTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 840
DB 811 ACCGCTTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 870
QY 841 GCTTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 900
DB 871 GCTTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 930
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QY 901 GAAGAAATGCTGAGAGAGAGCTCAGAGCTCAGGCTCCAGAGATGACATATCTGCACTC 960
DB 931 GAAGAAATGCTGAGAGAGAGCTCAGAGCTCAGGCTCCAGAGATGACATATCTGCACTC 990
QY 961 CTGCTCTGACTTCAAGCCGCTTACTTCCAAATATGAGAGAGCTCTGTAATACACCGCTCT 1020
DB 991 CTGCTCTGACTTCAAGCCGCTTACTTCCAAATATGAGAGAGCTCTGTAATACACCGCTCT 1050
QY 1021 GCCCAGGCTGATCTGAGCTGCTGTTTAAACAGACAGATGATGCTGATGAGAGAGCTC 1080
DB 1051 GCCCAGGCTGATCTGAGCTGCTGTTTAAACAGACAGATGATGCTGATGAGAGAGCTC 1110
QY 1081 CACACCTCTGACACACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1111 CACACCTCTGACACACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
QY 1141 GCGAGCGAGCTTTGATGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1171 GCGAGCGAGCTTTGATGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
QY 1201 AGTCTCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1231 AGTCTCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
QY 1261 GCCCTGTTTGGCTCTCTTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1291 GCCCTGTTTGGCTCTCTTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1350
QY 1321 AGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1351 AGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
QY 1381 ACTGAGAGCTTGAAGCTGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1411 ACTGAGAGCTTGAAGCTGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
QY 1441 GGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1471 GGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
QY 1501 TTTTAAATTAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAATTAAT 1552
RESULT 12
ADG89343
ID ADG89343 standard; DNA; 1552 BP.
XX
AC ADG89343;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cancer detection method related gene #6.
XX
KW ds; cancer; gene expression;
KW estrogen receptor-positive invasive breast cancer.
XX
OS Homo sapiens.
XX
PN MO2003078662-A1.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007713.
XX
PR 13-MAR-2002; 2002US-0364890P.
XX
PR 18-SEP-2002; 2002US-0412049P.
XX
PA (GENO-) GENOMIC HEALTH INC.
XX
PI Baker UB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX
```

DR MPI; 2003-767536/72.
XX Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.
XX
PS Disclosure; SEQ ID NO 291; 198bp; English.
XX
CC The invention relates to a method of predicting clinical outcome for a
CC patient diagnosed with cancer by determining the expression level of one
CC or more genes, or their expression products, selected from p53BP2,
CC cathepsin B, cathepsin L, Klf7/MiB1, and thymidine kinase in a cancer
CC tissue obtained from the patient, normalized against control gene(s), and
CC compared to the amount found in a reference cancer tissue set. The
CC specification also discloses an array comprising polynucleotides
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, SKI5, CEGP1, Ki-
CC 67, GSTM1, CA9, PR, BEC3, NME1, SURV, GAT3, TPRC, YB-1, DPYD, GSTM3,
CC RPS6KB1, Src, Chk1, ID1, Esrrb1, p27, CCNB1, XIAP, Chk2, CDC25B, IGFBP3,
CC AKO5699, PI3K2A, TGFBR3, BAG1, CYP3A4, BPCAM, VEGFR, p52, hENT1, WISP1,
CC HNF3A, NFKBp65, BRCA2, EGFR, TKI, VDR, Contis1037, pENT1, EPHX1, IRTA,
CC CDH1, HIF1c, IGFBP3, CTSE, Her2 and DIABLO, immobilized on a solid
CC surface. The methods are useful for predicting clinical outcome for a
CC patient diagnosed with cancer, classifying cancer, and predicting the
CC likelihood of long-term survival of a breast cancer patient, or a patient
CC diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC positive invasive breast cancer. This sequence corresponds to a gene
CC sequence whose expression is detected by the method of the invention.
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGATGCTCCCTGTCGCCAGCCCTGCTCTCTGTGTGATCCCGGCC 60
DB 31 ACAGTCAGCCGATGCTCCCTGTCGCCAGCCCTGCTCTCTGTGTGATCCCGGCC 90
QY 61 CCTGCTCCAGGCTCTCTGTGCACTGCTGCTGCTCTCTGTGATCCCGGCC 120
DB 91 CCTGCTCCAGGCTCTCTGTGCACTGCTGCTGCTCTCTGTGATCCCGGCC 150
QY 121 CCCCAAGGTTGCCCGATGAGAGGATTTCCCTTGGAGAGGCTCTCTGAGGGA 180
DB 151 CCCCAAGGTTGCCCGATGAGAGGATTTCCCTTGGAGAGGCTCTCTGAGGGA 210
QY 181 GATGACCCACTGCGCGAGAGGATCTGCCAGTGAAGAGATTCAACCCAGAGAGGAT 240
DB 211 GATGACCCACTGCGCGAGAGGATCTGCCAGTGAAGAGATTCAACCCAGAGAGGAT 270
QY 241 CCAACCCGAGAGAGATTAATCTTGAAGAGAGATTTACTCTGAGAGAGAGATTTACT 300
DB 271 CCAACCCGAGAGAGATTAATCTTGAAGAGAGATTTACTCTGAGAGAGAGATTTACT 330
QY 301 GAAGTTAAGCTTAATCAGAAAGAGAGCTCCCTGAAGTTAGAGATTTACTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAAAGAGAGCTCCCTGAAGTTAGAGATTTACTACTGTT 390
QY 361 GAGGCTCTGAGAGATCTTCAAGAACCCCAAGATTAATGCCACAGAGAGAGAGAT 420
DB 391 GAGGCTCTGAGAGATCTTCAAGAACCCCAAGATTAATGCCACAGAGAGAGAT 450
QY 421 GACCAAGATCATTTGGGCTATGAGAGGCAACCCGCTGAGCCCGGCTGCTCCCACTGC 480
DB 451 GACCAAGATCATTTGGGCTATGAGAGGCAACCCGCTGAGCCCGGCTGCTCCCACTGC 510
QY 481 GCGGCGCGCTTCCAGTCCCGGCTGATATCCGCCCCAGCTGCGGCTTCTGCCCCGAC 540
DB 511 GCGGCGCGCTTCCAGTCCCGGCTGATATCCGCCCCAGCTGCGGCTTCTGCCCCGAC 570
QY 541 CTGGGCGCGCTTCCAGTCTCTGAGGCTTTCAGCTCCCGGCTGCTCCAGAACTGCGGC 600
DB 571 CTGGGCGCGCTTCCAGTCTCTGAGGCTTTCAGCTCCCGGCTGCTCCAGAACTGCGGC 630

QY 601 AACCAATGCGCAGATGTGCACTGACCTGCTCTCTGAGCTAGAGATGCTGAGTCCC 660
DB 631 AACCAATGCGCAGATGTGCACTGACCTGCTCTCTGAGCTAGAGATGCTGAGTCCC 690
QY 661 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGAGGAGGCTGCAAGTGTCCGGCC 720
DB 691 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGAGGAGGCTGCAAGTGTCCGGCC 750
QY 721 TCGAGCACAATGTAAGAGCCACCTTCCCTGCGAGATCAGTGTGTTCACTGAC 780
DB 751 TCGAGCACAATGTAAGAGCCACCTTCCCTGCGAGATCAGTGTGTTCACTGAC 810
QY 781 ACCGCTTTGCCAGATTTGACAGAGGCTTGGGAGCCCGGAGAGGCTGAGTGGCC 840
DB 811 ACCGCTTTGCCAGATTTGACAGAGGCTTGGGAGCCCGGAGAGGCTGAGTGGCC 870
QY 841 GCGCTTCTGAGAGAGGCGCGGAGAGAAACAGTGTGTTAGAGAGTGTGCTGCTTGG 900
DB 871 GCGCTTCTGAGAGAGGCGCGGAGAGAAACAGTGTGTTAGAGAGTGTGCTGCTTGG 930
QY 901 GAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGCTGACATATCTGACTC 960
DB 931 GAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGCTGACATATCTGACTC 990
QY 961 CTGCGCTTCTGACTCAGCGCTTACTTCCATATGAGGAGTCTTGTACTACACCGCTGT 1020
DB 991 CTGCGCTTCTGACTCAGCGCTTACTTCCATATGAGGAGTCTTGTACTACACCGCTGT 1050
QY 1021 GCCCAAGGTCATCTGAGCTGATGTTTAAACAGACAGTGAAGCTGAGAGCTGAGAGCTC 1080
DB 1051 GCCCAAGGTCATCTGAGCTGATGTTTAAACAGACAGTGAAGCTGAGAGCTGAGAGCTC 1110
QY 1081 CACAACCTCTCTGACACCTGTGAGGACCTGTGATCTCTCGGCTACACGCTGAACCTCCGA 1140
DB 1111 CACAACCTCTCTGACACCTGTGAGGACCTGTGATCTCTCGGCTACACGCTGAACCTCCGA 1170
QY 1141 GCGAGCAGCTTGTGAATGAGCGAGTGAAGTGAAGCTCTTCTCTGAGTGAAGCAGC 1200
DB 1171 GCGAGCAGCTTGTGAATGAGCGAGTGAAGTGAAGCTCTTCTCTGAGTGAAGCAGC 1230
QY 1201 AGTCTCGGAGCTGAGCGCAGTCAAGCTGAATTCGAGCTGAGCTGAGTGAACCTCTA 1260
DB 1231 AGTCTCGGAGCTGAGCGCAGTCAAGCTGAATTCGAGCTGAGCTGAGTGAACCTCTA 1290
QY 1261 GCCCTGTTTGGCTCTTCTTGTGCTCAACAGCGTCCGCTCTTGTGCAATGAGA 1320
DB 1291 GCCCTGTTTGGCTCTTCTTGTGCTCAACAGCGTCCGCTCTTGTGCAATGAGA 1350
QY 1321 AGGCAAGCAGAGAGGAGAACCAAGGGGCTGTGAGCTACCGCCAGAGAGTACCGAG 1380
DB 1351 AGGCAAGCAGAGAGGAGAACCAAGGGGCTGTGAGCTACCGCCAGAGAGTACCGAG 1410
QY 1381 ACTGAGAGCTGAGAGGCTGATCTTGAAGATGTGAAGAGCCAGAGAGAGGATCTGAGG 1440
DB 1411 ACTGAGAGCTGAGAGGCTGATCTTGAAGATGTGAAGAGCCAGAGAGGATCTGAGG 1470
QY 1441 GAGCGCGTAACTGTCTCTCTGCTCAATATGCACTTCTTTTAACTGCGCAAGAAAT 1500
DB 1471 GAGCGCGTAACTGTCTCTCTGCTCAATATGCACTTCTTTTAACTGCGCAAGAAAT 1530
QY 1501 TTTTAAATTAATTTTAAAT 1522
DB 1531 TTTTAAATTAATTTTAAAT 1552
RESULT 13
ACC72730
ID ACC72730 standard; cdna; 1552 BP.
XX ACC72730;
XX
DT 09-JUL-2003 (first entry)

XX DE Human cancer related protein encoding cDNA SEQ ID NO:69.
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW heart disease; atherosclerosis; endometriosia; gene; ss.
XX OS Homo sapiens.
XX XX MO2003025138-A2.
XX PN 27-MAR-2003.
XX PD 17-SEP-2002; 2002WO-US029560.
XX PF 17-SEP-2001; 2001US-0323469P.
XX PR 20-SEP-2001; 2001US-0323887P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 08-FEB-2002; 2002US-0355145P.
XX PR 08-FEB-2002; 2002US-0355257P.
XX PR 12-APR-2002; 2002US-0372246P.
XX XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA Afar D, Aziz N, Glen KC, Hevezi PA, Mack DH, Wilson KE;
XX PI Zlotnick A;
XX XX WPI, 2003-354600/33.
XX DR P-PSDB; ABR58595.
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart disease, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX PS Claim 8; Page 662; 767P; English.
XX XX The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR58521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischemia, heart disease,
XX CC atherosclerosis and endometriosia. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX XX Sequence 1552 BP, 302 A, 471 C, 461 G, 318 T, 0 U, 0 Other;
SQ

QY 181 GATGACCACTGGGCGAGAGGATCTGCCAGTGAAGAGAGATTACCCAGAGAGAGAT 240
Db 211 GATGACCACTGGGCGAGAGGATCTGCCAGTGAAGAGAGATTACCCAGAGAGAGAT 270
QY 241 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
Db 271 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 360
Db 331 GAAGTTAAGCTTAATCAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 390
QY 361 GAGGCTCCGAGATCTCAAGAACCCGAGATTAATGCCACAGGAGCAAGAGAGGAGAT 420
Db 391 GAGGCTCCGAGATCTCAAGAACCCGAGATTAATGCCACAGGAGCAAGAGAGGAGAT 450
QY 421 GACAGAGTCAATTTGGCTATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 451 GACAGAGTCAATTTGGCTATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
QY 481 GCGGAGCGCTTCAAGTCCCGGATATCCCGGATATCCCGGATATCCCGGATATCCCGG 540
Db 511 GCGGAGCGCTTCAAGTCCCGGATATCCCGGATATCCCGGATATCCCGGATATCCCGG 570
QY 541 CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGGCTCCAGAGATCGGCGCTGGCG 600
Db 571 CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGGCTCCAGAGATCGGCGCTGGCG 630
QY 601 AACCAATGACCAAGTGTGCACTGACCTGCTCTGCTGAGATGAGTCTGAGTCTCC 660
Db 631 AACCAATGACCAAGTGTGCACTGACCTGCTCTGCTGAGATGAGTCTGAGTCTCC 690
QY 661 GGGCGGAGATCCGGGCTTGTGAGCTGATCTGCACTGGGGGCTGCAAGTGTCTGGG 720
Db 691 GGGCGGAGATCCGGGCTTGTGAGCTGATCTGCACTGGGGGCTGCAAGTGTCTGGG 750
QY 721 TGGAGACACATGTGGAAGGACACCGTTCCCTGCCAGATCCAGTGTGATCACTCAGC 780
Db 751 TGGAGACACATGTGGAAGGACACCGTTCCCTGCCAGATCCAGTGTGATCACTCAGC 810
QY 781 ACCGCTTTGACAGATTTGACAGAGGCTTGGGGGCTGAGAGGCTGAGCGTGTGGC 840
Db 811 ACCGCTTTGACAGATTTGACAGAGGCTTGGGGGCTGAGAGGCTGAGCGTGTGGC 870
QY 841 GCGTTTCTGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGAGTTCGTCTGCTTG 900
Db 871 GCGTTTCTGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGAGTTCGTCTGCTTG 930
QY 901 GAAGAAATGCTGAGAGAGGCTCAAGAGATCAAGTCCAGAGCTGAGCAATATCTGACATC 960
Db 931 GAAGAAATGCTGAGAGAGGCTCAAGAGATCAAGTCCAGAGCTGAGCAATATCTGACATC 990
QY 961 CTGCGCTTGAATTCAGCGGCTACTTCAATATGAGAGGCTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCGCTTGAATTCAGCGGCTACTTCAATATGAGAGGCTCTCTGACTACACCGCCCTGT 1050
QY 1021 GCCCAGGATGTCAATCTGACCTGTGTTAAACAGACAGTATGCTGATGAACAGCTTC 1080
Db 1051 GCCCAGGATGTCAATCTGACCTGTGTTAAACAGACAGTATGCTGATGAACAGCTTC 1110
QY 1081 CACACCTTCTGACACCTCTGAGGAGACCTGAGTACTCTCCGCTAACAGTGAACCTTCCGA 1140
Db 1111 CACACCTTCTGACACCTCTGAGGAGACCTGAGTACTCTCCGCTAACAGTGAACCTTCCGA 1170
QY 1141 GCGAGCAGACCTTTGATGATGAGGAGTGAAGGCTCTCTCCCTGCTGAGTGAACAGC 1200
Db 1171 GCGAGCAGACCTTTGATGATGAGGAGTGAAGGCTCTCTCCCTGCTGAGTGAACAGC 1230
QY 1201 AGTCTCGGAGCTGTGAGGCAAGTCCAGCTGAATTCCTGCTGAGCTGTGATCATCTTA 1260
Db 1231 AGTCTCGGAGCTGTGAGGCAAGTCCAGCTGAATTCCTGCTGAGCTGTGATCATCTTA 1290

QY 1261 GCCCTGGTTTTGGCCCTTTTGGCTGCACAGGGGTGGCTTCTGTGCGAGATGAGA 1320
DB 1291 GCCCTGGTTTTGGCCCTTTTGGCTGCACAGGGGTGGCTTCTGTGCGAGATGAGA 1350
QY 1321 AGGCACACAGAGAGGGGAAACCAAGGGGGGTGTAGCTACCGCCACAGAGGTAGCCGAG 1380
DB 1351 AGGCACACAGAGAGGGGAAACCAAGGGGGGTGTAGCTACCGCCACAGAGGTAGCCGAG 1410
QY 1381 ACTGGAGCTTGAAGGCTGTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGCATCTGAGG 1440
DB 1411 ACTGGAGCTTGAAGGCTGTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGCATCTGAGG 1470
QY 1441 GGAGCCGGTAACTGCTGCTGCTCATATGACACTTCTTTAAGTCCCAAGAAAT 1500
DB 1471 GGAGCCGGTAACTGCTGCTGCTCATATGACACTTCTTTAAGTCCCAAGAAAT 1530
QY 1501 TTTTAAATAAATATTTATTAAT 1522
DB 1531 TTTTAAATAAATATTTATTAAT 1552

RESULT 14
ABZ77284
ID ABZ77284 standard; cDNA; 1552 BP.
XX
AC ABZ77284;
DT 28-MAY-2003 (first entry)
XX
DE Nucleotide sequence of human CA9 polypeptide.
XX
KM Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
folicular development; CA9; HXB; IGFBP5; HFAFP; STC1; mlg-6; SSR4;
cancer; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..1422
FT /tag= a
FT /product= "CA9"
XX
PN MO2003010205-A1.
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-US023786.
XX
PR 26-JUL-2001; 2001US-0307600P.
PR 24-JUL-2002; 2002US-00201642.
XX
PA (UYDU-) UNIV DUKE MEDICAL CENT.
XX
PI Riggle GJ, Lal A;
XX
DR MPI: 2003-239423/23.
DR P-PSDB; ABP9744.
XX
PT Inhibiting angiogenesis for treating wound healing, retinopathy,
ischemia, inflammation, microvasculopathy, bone healing, skin
PT inflammation or folicular development by providing to a subject an
PT antisense polynucleotide.
XX
PS Claim 1; Page 47; 66pp; English.
XX
CC The present sequence encodes a human CA9 polypeptide. It is used in the
method of the invention. The specification describes a method modulating
CC angiogenesis associated with wound healing, retinopathy, ischemia,
CC inflammation, microvasculopathy, bone healing, skin inflammation or
CC folicular development. The method comprises providing to a subject HOG3,
CC HOG8, HOG18, CA9, HXB, IGFBP5, HFAFP, STC1, mlg-6 or SSR4. The methods,
CC antisense polynucleotides, polypeptides and antibodies are useful for

CC treating wound healing, retinopathy, ischemia, inflammation,
CC microvasculopathy, bone healing, skin inflammation or folicular
CC development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTACCCGATGCTCCCTGTGCCCCAGCCCTGGCTCCCTGTGATCCCGGCC 60
DB 31 ACAGTACCCGATGCTCCCTGTGCCCCAGCCCTGGCTCCCTGTGATCCCGGCC 90
QY 61 CCTGTCCAGGCTTCACTGTGCACTGTGCTGTGCTGTGCTGTGATGCTGTGAT 120
DB 91 CCTGTCCAGGCTTCACTGTGCACTGTGCTGTGCTGTGCTGTGATGCTGTGAT 150
QY 121 CCCAGAGTTGCCCTGGATGAGAGGATTTCCCTTGGAGAGGCTTTTGGGAA 180
DB 151 CCCAGAGTTGCCCTGGATGAGAGGATTTCCCTTGGAGAGGCTTTTGGGAA 210
QY 181 GATGACCCACTGGGCGAGAGGATCTGCCATGTGAAGGATTTCACCAGAGAGGAT 240
DB 211 GATGACCCACTGGGCGAGAGGATCTGCCATGTGAAGGATTTCACCAGAGAGGAT 270
QY 241 CCACCCGAGAGAGGATCTACTGTGAGAGGATCTACTGTGAGAGGATCTACT 300
DB 271 CCACCCGAGAGAGGATCTACTGTGAGAGGATCTACTGTGAGAGGATCTACT 330
QY 301 GAAGTTAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTTAGAGATCTTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTTAGAGATCTTACTGTT 390
QY 361 GAGGCTCTGAGAGATCTCTCAAGAAACCCAGAAATATATGCCACAGGACAAAGAGGAT 420
DB 391 GAGGCTCTGAGAGATCTCTCAAGAAACCCAGAAATATATGCCACAGGACAAAGAGGAT 450
QY 421 GACCAAGTCAATGGCGCTATGAGAGCGACCCGCTTGGCCCGGATGCCAGCCTGC 480
DB 451 GACCAAGTCAATGGCGCTATGAGAGCGACCCGCTTGGCCCGGATGCCAGCCTGC 510
QY 481 GCGGCGGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGGCCCTTTCGCCCGGCC 540
DB 511 GCGGCGGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGGCCCTTTCGCCCGGCC 570
QY 541 CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGGC 600
DB 571 CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGGC 630
QY 601 AACCAATGGCCACAGTGTGCAACTGACCTGTGCTTGGGCTTGAAGATGCTTGGGATCC 660
DB 631 AACCAATGGCCACAGTGTGCAACTGACCTGTGCTTGGGCTTGAAGATGCTTGGGATCC 690
QY 661 GGGCGGAGTACCGGGCTTCTGCACTGATGCACTGTGAGAGGCTTGGAGGCTTCCGGGC 720
DB 691 GGGCGGAGTACCGGGCTTCTGCACTGATGCACTGTGAGAGGCTTGGAGGCTTCCGGGC 750
QY 721 TCGAGACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCAGTGTTCACCTCAGC 780
DB 751 TCGAGACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCAGTGTTCACCTCAGC 810
QY 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGAGGCGCCCGGAGGCTTGGCGTTGGCC 840
DB 811 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGAGGCGCCCGGAGGCTTGGCGTTGGCC 870
QY 841 GCTTTTCTGAGAGAGGCGCCGGAAGAAACAGTCCCTTATGAGCATGTTGCTTCCGCTTG 900
DB 871 GCTTTTCTGAGAGAGGCGCCGGAAGAAACAGTCCCTTATGAGCATGTTGCTTCCGCTTG 930
QY 901 GAAAGAAATCGTGAAGAGGCTCAGAGACTCAGGTCCAGAGCTGAGCATATCTGCACTC 960

Db 931 GAAGAAATGCTGAGGAGAGCTCAGAGACTCAGGTCCAGAGACTGAGCATATCTGCATTC 990
Qy 961 CTGGCCCTGAGCTTGAGCGGCTACTTCCATATAGAGGGGTCTGACTACCGCCCTGT 1020
Db 991 CTGGCCCTGAGCTTGAGCGGCTACTTCCATATAGAGGGGTCTGACTACCGCCCTGT 1050
Qy 1021 GCCCAGGGGTGATCTGAGCTGTGTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1080
Db 1051 GCCCAGGGGTGATCTGAGCTGTGTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTTGGCTACAGCTGAACCTTCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTTGGCTACAGCTGAACCTTCCGA 1170
Qy 1141 GGGAGCAGCCTTTGAAATGGGGAGTGAATGAGGCTCTCTCCCTGCTGAGAGTGAACAGC 1200
Db 1171 GGGAGCAGCCTTTGAAATGGGGAGTGAATGAGGCTCTCTCCCTGCTGAGAGTGAACAGC 1230
Qy 1201 AGTCTCTGGGCTGCTGAGCAGCTCAGCTGAATTCCTGCTGGCTGCTGATCATCTTA 1260
Db 1231 AGTCTCTGGGCTGCTGAGCAGCTCAGCTGAATTCCTGCTGGCTGCTGATCATCTTA 1290
Qy 1261 GCCCTGGTTTTTGGCCTCTTTTGTCTGTACACAGCGTGGCTTCTTGTGAGATGAGA 1320
Db 1291 GCCCTGGTTTTTGGCCTCTTTTGTCTGTACACAGCGTGGCTTCTTGTGAGATGAGA 1350
Qy 1321 AGGCAGCAGAGAGGGGAAACCAAGGGGTGTGAGTACCCGCCAGACAGGTAGCCGAG 1380
Db 1351 AGGCAGCAGAGAGGGGAAACCAAGGGGTGTGAGTACCCGCCAGACAGGTAGCCGAG 1410
Qy 1381 ACTGAGCCTTGAAGGCTGTGATCTTGAAGATGTGAGAGCCAGACGAGGATCTGAGGG 1440
Db 1411 ACTGAGCCTTGAAGGCTGTGATCTTGAAGATGTGAGAGCCAGACGAGGATCTGAGGG 1470
Qy 1441 GAGAGCGGTACTGTCTGTCTCTCTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1500
Db 1471 GAGAGCGGTACTGTCTGTCTCTCTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1530
Qy 1501 TTTTAAATTAATATTTATTAAT 1522
Db 1531 TTTTAAATTAATATTTATTAAT 1552

RESULT 15
ADN39704
ID ADN39704 standard; cDNA, 1552 BP.
XX
AC ADN39704;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C76.
XX
KM Human; differential expression; cancer; angiogenic disorder;
XX
KM fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
XX
KM inflammatory disease; autoimmune disease; scarring; uterine fibroid;
XX
KM retinal neovascularization syndrome; prognosis; drug screening; drug targeting;
XX
KM wound healing; contraception; cytostatic; candiant; immunomodulatory;
XX
KM vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0355714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368099P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397755P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Heverzi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR MPI; 2003-468649/44.
XX
PT P-PSDB; ADN39921.
XX
PT Determining the presence or absence of a pathological cell in a patient,
XX
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO C76; 1385bp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularization syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 11; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCGCGATGAGTCCCTGTGAGCCAGCCCTGGCTCCCTGTGATCCGAGCC 60
Db 31 AAGATCAGCGCGATGAGTCCCTGTGAGCCAGCCCTGGCTCCCTGTGATCCGAGCC 90
Qy 61 CCTGTCCAGGCTCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACT 120
Db 91 CCTGTCCAGGCTCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACT 150
Qy 121 CCCAGAGGTTGCCCCGAGATGAGAGATTTCCCTGGGAGAGGCTCTTGGGGAA 180
Db 151 CCCAGAGGTTGCCCCGAGATGAGAGATTTCCCTGGGAGAGGCTCTTGGGGAA 210
Qy 181 GATGACCCACTGGGAGAGAGATCTGCCAGATGAAGAGATTCAACCCAGAGAGAGAT 240
Db 211 GATGACCCACTGGGAGAGAGATCTGCCAGATGAAGAGATTCAACCCAGAGAGAGAT 270
Qy 241 CCACCCGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCT 300
Db 271 CCACCCGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCT 330

QY 301 GAAGTTAAGCTTAATCAAGAAAGAGGGCTCCCTGAAATTAGAGATCTACTATGTT 360
DB 331 GAAGTTAAGCTTAATCAAGAAAGAGGGCTCCCTGAAATTAGAGATCTACTATGTT 390
QY 361 GAGGCTCTGAGATCTCTCAAGAACCCAGATATATGCCCAGGGGCAAGAAAGGGGAT 420
DB 391 GAGGCTCTGAGATCTCTCAAGAACCCAGATATATGCCCAGGGGCAAGAAAGGGGAT 450
QY 421 GACCAAGATCATTTGGGCTATGAGAGCGACCCGCTGAGCCCGGGGTCTCCAGGCTGC 480
DB 451 GACCAAGATCATTTGGGCTATGAGAGCGACCCGCTGAGCCCGGGGTCTCCAGGCTGC 510
QY 481 GCGGGCGGCTTCCAGTCCCGGCTGATATCCGCCCCAGTCCGCCCCCTTCTGCCCCGGCC 540
DB 511 GCGGGCGGCTTCCAGTCCCGGCTGATATCCGCCCCAGTCCGCCCCCTTCTGCCCCGGCC 570
QY 541 CTGCGCCCCCTGGAATCTCTGAGCTTCAAGCTCCGCGCGCTCCAGAACTGCGGCTGCGC 600
DB 571 CTGCGCCCCCTGGAATCTCTGAGCTTCAAGCTCCGCGCGCTCCAGAACTGCGGCTGCGC 630
QY 601 AACCAATGSCCAAGTGTGCAACTGACCTGCTCTGAGCTAGAGATGAGCTTGGGTCCC 660
DB 631 AACCAATGSCCAAGTGTGCAACTGACCTGCTCTGAGCTAGAGATGAGCTTGGGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGAGCTGCACTGCACTTGGGGGGCTGCAAGTCTGCGGGC 720
DB 691 GGGCGGGAGTACCGGGCTCTGAGCTGCACTGCACTTGGGGGGCTGCAAGTCTGCGGGC 750
QY 721 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCCAGATCCACGTGTTCACTCAGC 780
DB 751 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCCAGATCCACGTGTTCACTCAGC 810
QY 781 ACCGCTTTTGGCAGAGTTGACAGGCTTGGGGGCTCCGAGAGGCTTGGCTTGGTGC 840
DB 811 ACCGCTTTTGGCAGAGTTGACAGGCTTGGGGGCTCCGAGAGGCTTGGCTTGGTGC 870
QY 841 GCCTTCTGAGAGGGGCCCGAGAAACAAGTGCCTATGAGAGTGTGCTGCTGCTG 900
DB 871 GCCTTCTGAGAGGGGCCCGAGAAACAAGTGCCTATGAGAGTGTGCTGCTGCTG 930
QY 901 GAAGAAATGCTGAGAGAGGCTCAGAGCTCAGTCCAGAGCTGAGCATATCTGACATC 960
DB 931 GAAGAAATGCTGAGAGAGGCTCAGAGCTCAGTCCAGAGCTGAGCATATCTGACATC 990
QY 961 CTGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGTACTACACCCGCTGT 1020
DB 991 CTGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGTACTACACCCGCTGT 1050
QY 1021 GCCCAGGGTGTATCTGAGCTGTGTTTACAGACAGATGATGCTAGTCTAAGCAGCTC 1080
DB 1051 GCCCAGGGTGTATCTGAGCTGTGTTTACAGACAGATGATGCTAGTCTAAGCAGCTC 1110
QY 1081 CACACCTCTCTGACACCTCTGTGGGGAAGCTGAGTCTGCGCTACAGCTGAATTTCCGA 1140
DB 1111 CACACCTCTCTGACACCTCTGTGGGGAAGCTGAGTCTGCGCTACAGCTGAATTTCCGA 1170
QY 1141 GGGAGGCACTTTGAATGGGCGAGTGAATGAGGCTCTTCTGCTGAGTGAAGCAGC 1200
DB 1171 GGGAGGCACTTTGAATGGGCGAGTGAATGAGGCTCTTCTGCTGAGTGAAGCAGC 1230
QY 1201 AGTCTCTGGGGCTGAGGCACTGAGTGAATTCCTGCTGAGTGAAGCAGTCTA 1260
DB 1231 AGTCTCTGGGGCTGAGGCACTGAGTGAATTCCTGCTGAGTGAAGCAGTCTA 1290
QY 1261 GCGCTGTTTGGCTCTCTTTTGGTGTACACAGAGTGCAGTCTCTTGTGCAATGAGA 1320
DB 1291 GCGCTGTTTGGCTCTCTTTTGGTGTACACAGAGTGCAGTCTCTTGTGCAATGAGA 1350
QY 1321 AGGCAAGCAAGAAAGGGGAAACAAAGGGGTGTGAGTACCGCCAGCAGAGTACCGAG 1380
DB 1351 AGGCAAGCAAGAAAGGGGAAACAAAGGGGTGTGAGTACCGCCAGCAGAGTACCGAG 1410
QY 1381 ACTGAGGCTTGAAGGCTGAGTCTTGGAGATGTGAGAAAGCCAGCCAGAGGCTTGAAGG 1440

DB 1411 ACTGAGGCTTGAAGGCTGAGTCTTGGAGATGTGAGAAAGCCAGAGGCAATCTGAGGG 1470
QY 1441 GAGAGCGGTAACTGTCTGTCTGCTCATTAATGCCACTTCTTTAACTGCCAAGAAAT 1500
DB 1471 GAGAGCGGTAACTGTCTGTCTGCTCATTAATGCCACTTCTTTAACTGCCAAGAAAT 1530
QY 1501 TTTTAAATTAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAATTAAT 1552

Search completed: February 6, 2005, 07:47:18
Job time : 737 secs

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Db	1	ACAGTCACGCCGATGAGCTCCCTCTGTCACGCTGCTGTCATCCGAGC	60
QY	61	CTGTGCTCCAGGCTCTCACTGTGCAACTGTCTGTCACTGTGCTTGTGATGCTGTCTCAT	120
Db	61	CTGTGCTCCAGGCTCTCACTGTGCAACTGTCTGTCTGTGATGCTGTCTCAT	120
QY	121	CCCCAGAGGTTGCCCCCGGATGCAAGAGGATTTCCCCCTTGTGGAGAGAGGCTCTTCTGGAGAA	180
Db	121	CCCCAGAGGTTGCCCCCGGATGCAAGAGGATTTCCCCCTTGTGGAGAGAGGCTCTTCTGGAGAA	180
QY	181	GATGACCCCATCTGGGCGAGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT	240
Db	181	GATGACCCCATCTGGGCGAGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT	240
QY	241	CAACCCCGAGAGAGAGATTTACTGTGAGAGAGAGATCTTACTGTGAGAGAGATTTACT	300
Db	241	CAACCCCGAGAGAGAGATTTACTGTGAGAGAGAGATTTACTGTGAGAGAGATTTACT	300
QY	301	GAAGTTTAAGCTTAATCAGAAAGAAGGAGCTCCCTGAAGTTTGAAGGATTTACTACTGTT	360
Db	301	GAAGTTTAAGCTTAATCAGAAAGAAGGAGCTCCCTGAAGTTTGAAGGATTTACTACTGTT	360
QY	361	GAGGCTCTTGAGGATCTTCAAGAAACCCCAAGATTAATGCCACAGGAGCAAAAGAGGAGT	420
Db	361	GAGGCTCTTGAGGATCTTCAAGAAACCCCAAGATTAATGCCACAGGAGCAAAAGAGGAGT	420
QY	421	GACCAAGATCAATTGGGCTATGGAAGCGACCCGCTGGCCCGGGTGTGCCAGCTGAC	480
Db	421	GACCAAGATCAATTGGGCTATGGAAGCGACCCGCTGGCCCGGGTGTGCCAGCTGAC	480
QY	481	GCGGGCGGCTTCCAGTCCCGGATGATATCCGCCCCAGCTGCGGCTTCTTCCCGGAGC	540
Db	481	GCGGGCGGCTTCCAGTCCCGGATGATATCCGCCCCAGCTGCGGCTTCTTCCCGGAGC	540
QY	541	CTGGGCCCCCTTGGAACTCTTGGGGCTTCCAGGCTCCGCGGCTTCCAGAACTTGGGCTTGGC	600
Db	541	CTGGGCCCCCTTGGAACTCTTGGGGCTTCCAGGCTCCGCGGCTTCCAGAACTTGGGCTTGGC	600
QY	601	AACATAGGCACAGTGTGCACTGACCCCTGCTCTGGGCTTGAAGATGGCTCTTGGGCTCC	660
Db	601	AACATAGGCACAGTGTGCACTGACCCCTGCTCTGGGCTTGAAGATGGCTCTTGGGCTCC	660
QY	661	GGGCGGAGATCCGGGCTCTGCACTGTGCACTGTGCACTGGGGGGGCTGTGCACTGTCCGGGCT	720
Db	661	GGGCGGAGATCCGGGCTCTGCACTGTGCACTGTGCACTGGGGGGGCTGTGCACTGTCCGGGCT	720
QY	721	TCGAGGACACATGTGGAAGGACACCGGTTCCCTGTGCGAGATCCAGTGTGCTCACTCAACG	780
Db	721	TCGAGGACACATGTGGAAGGACACCGGTTCCCTGTGCGAGATCCAGTGTGCTCACTCAACG	780
QY	781	ACCGGCTTTCGCAAGATTGACGAGGCTTGGGGGCGCCCGGAGAGGCTGTGCTGTGTGGCC	840
Db	781	ACCGGCTTTCGCAAGATTGACGAGGCTTGGGGGCGCCCGGAGAGGCTGTGCTGTGTGGCC	840
QY	841	GCCCTTTCGAGAGAGAGGCGCCCGGAAGAAACAATGTGCTATGAGCAATGTGTCTGTGGCTTG	900
Db	841	GCCCTTTCGAGAGAGAGGCGCCCGGAAGAAACAATGTGCTATGAGCAATGTGTCTGTGGCTTG	900
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Db	901	GAAGAAATCGCTGAGAGAGAGGCTCAAGACTCAGATCCAGAGCTGAGCAATATCTGCACTTC	960
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Qy	1081	CACACCCCTCTGTGACACCCCTGTGGGAGACCTGGTGACTCTGGGCTACAGCTAACTTCCGA	11448
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Db	1321	AGGCGACACAGAAAGGGGAAACMAAGGGGGGTGTGAGCTACCGGCCACAGCAGAGTATGCCGAG	1380
Qy	1381	ACTGAGACCTTAGAGGCTGTGATCTTGTGAGAAATGTGAGAAGCAGGCGACAGAGGCACTGTGAGGG	1440
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Qy	1441	GGAGCCGGGTAACTGTCTGTCTGTGCTCATTTATATGCGCACTTCTTTTAACTGTGCCAAGAAAT	1500
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Db	1501	TTTTTAAATTAATTTTATTAAT	1522

RESULT 2
 US-08-477-504A-1
 Sequence 1, Application US/08477504A
 Patent No. 5972353
 GENERAL INFORMATION:
 APPLICANT: Zavada, Jan
 APPLICANT: Pastorekova, Silvia
 APPLICANT: Pastorek, Jaromir
 TITLE OF INVENTION: MN Gene and Protein
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leona L. Lauder
 STREET: 6 Mariposa Court
 CITY: Tiburon
 STATE: California
 COUNTRY: USA
 ZIP: 94920
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,504A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/260,190
 FILING DATE: 15-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lauder, Leona L.
 REGISTRATION NUMBER: 30,863
 REFERENCE/DOCKET NUMBER: D-0021.3D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-435-2034
 TELEFAX: 415-435-0727
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1522 base pairs
 type: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-477-504A-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1501 TTTTAAATTAATTTTAAAT 1522

RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Laufer
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
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NAME: lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Query Match 100.0% Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-08-485-862B-1
; Sequence 1, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: NM Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-862B-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTACGCGCATGCTCCCTGTCGCCCAAGCCCTGCTCCCTGTGTTATCCCGGCC 60
DB 1 AAGTCAGCGCATGCTCCCTGTCGCCCAAGCCCTGCTCCCTGTGTTATCCCGGCC 60
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DB 721 TGGGAGCACAATGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 780
QY 781 ACCGCTTTCAGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 840
DB 781 ACCGCTTTCAGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 840
QY 841 GCTTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 900
DB 841 GCTTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 900
QY 901 GAAGAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 960
DB 901 GAAGAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 960
QY 961 CTGCGCTCTGACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1020
DB 961 CTGCGCTCTGACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1020
QY 1021 GCCAGAGGTCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1080
DB 1021 GCCAGAGGTCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1080
QY 1081 CACACCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1140
DB 1081 CACACCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1140
QY 1141 GCGAGCAGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1200
DB 1141 GCGAGCAGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1200
QY 1201 AGTCTCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1260
DB 1201 AGTCTCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1260
QY 1261 GCGCTGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
DB 1261 GCGCTGCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 AGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
DB 1321 AGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
QY 1381 ACTGAGCTTGAAGCTGAGATCTTGAAGATGAGAGAGAGAGAGAGAGAT 1440
DB 1381 ACTGAGCTTGAAGCTGAGATCTTGAAGATGAGAGAGAGAGAGAGAGAT 1440
QY 1441 GAGAGCGGTAATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
DB 1441 GAGAGCGGTAATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
QY 1501 TTTTAAATTAATTTATTAAT 1522
DB 1501 TTTTAAATTAATTTATTAAT 1522

RESULT 5
US-08-787-739-1
Sequence 1, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-787-739-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAAGCCGATGCTCCCTGATGCCCCAGCCCTGCTCCCTGTGTTAGTCCGAGC 60
DB 1 AAGATCAAGCCGATGCTCCCTGATGCCCCAGCCCTGCTCCCTGTGTTAGTCCGAGC 60
QY 61 CCTGCTCAAGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CCGTCCAGCCGCTCACTGCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCCGAGAGGTTTCCCGGATGAGAGGATTTCCCTTTGGAGAGAGGCTCTTCTGGGAA 180
DB 121 CCCGAGAGGTTTCCCGGATGAGAGGATTTCCCTTTGGAGAGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240

DB 181 GATGACCCACTGGGCGAGAGATTTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
QY 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTACCT 300
DB 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTACCT 300
QY 301 GAAATTAAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTTAGAGATCTACTCTGT 360
DB 301 GAAATTAAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTTAGAGATCTACTCTGT 360
QY 361 GAGGCTCTGAGAGATCTCAAGAAACCCAGATAATGCCCCACAGAGACAAAGAGGAT 420
DB 361 GAGGCTCTGAGAGATCTCAAGAAACCCAGATAATGCCCCACAGAGACAAAGAGGAT 420
QY 421 GACAGAGTCAATGGCGCTATGAGAGCGACCCGCTGAGCCCTCCGAGCTGAC 480
DB 421 GACAGAGTCAATGGCGCTATGAGAGCGACCCGCTGAGCCCTCCGAGCTGAC 480
QY 481 GGGGCGGCTTCCAGTCCCGGCTGATATCCGCCCCAGCTTCCGCTTCTGCCCCGCC 540
DB 481 GGGGCGGCTTCCAGTCCCGGCTGATATCCGCCCCAGCTTCCGCTTCTGCCCCGCC 540
QY 541 CTGGCCCCCTGGAATCTCTGAGGCTTCCAGCTCCCGGCTCCAGAACTGGCTGGCC 600
DB 541 CTGGCCCCCTGGAATCTCTGAGGCTTCCAGCTCCCGGCTCCAGAACTGGCTGGCC 600
QY 601 AACAATGGCCACAGTGTGCAACTGACCTGCTCTGAGGCTGAGAGATGGCTGGGCTCC 660
DB 601 AACAATGGCCACAGTGTGCAACTGACCTGCTCTGAGGCTGAGAGATGGCTGGGCTCC 660
QY 661 GGGCGGAGTACCGGCTCTGAGCTGATGCACTGGAGGGGCTGAGGCTGCTGGGCG 720
DB 661 GGGCGGAGTACCGGCTCTGAGCTGATGCACTGGAGGGGCTGAGGCTGCTGGGCG 720
QY 721 TCGAGCACTGTTGGAAGGCAACCGTTCCCTGCGAGATCAAGTGTTCACCTGAC 780
DB 721 TCGAGCACTGTTGGAAGGCAACCGTTCCCTGCGAGATCAAGTGTTCACCTGAC 780
QY 781 ACCGCTTTCGAGAGTGAAGAGGCTTGGAGGCGCCGAGAGGCTGGCGGTGGCC 840
DB 781 ACCGCTTTCGAGAGTGAAGAGGCTTGGAGGCGCCGAGAGGCTGGCGGTGGCC 840
QY 841 GCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTATGAGAGTCTGCTGCTG 900
DB 841 GCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTATGAGAGTCTGCTGCTG 900
QY 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCACAGACTGACATATCTGCACTC 960
DB 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCACAGACTGACATATCTGCACTC 960
QY 961 CTGCTCTGACTTCAAGCGCTCACTTCCATATGAGGAGTCTGACTACACCGCTGT 1020
DB 961 CTGCTCTGACTTCAAGCGCTCACTTCCATATGAGGAGTCTGACTACACCGCTGT 1020
QY 1021 GCCAGAGGTGTCATGAGCTGTGTTTAAACAGACAGTGAAGTGAAGGCTTAAGAGCTC 1080
DB 1021 GCCAGAGGTGTCATGAGCTGTGTTTAAACAGACAGTGAAGTGAAGGCTTAAGAGCTC 1080
QY 1081 CACACCTCTCTGACACCTGTGGGAGACTGTGATCTCTCGCTACACCTGAATCTTCCGA 1140
DB 1081 CACACCTCTCTGACACCTGTGGGAGACTGTGATCTCTCGCTACACCTGAATCTTCCGA 1140
QY 1141 GCGAGCAGCTTGAATGAGGAGTGAAGGCTCTTCTGCTGAGTGAAGCAGC 1200
DB 1141 GCGAGCAGCTTGAATGAGGAGTGAAGGCTCTTCTGCTGAGTGAAGCAGC 1200
QY 1201 AGTCTGAGGCTGAGAGCAGTCAAGTGAATTCGCTGAGGCTGAGTGAATCTCTA 1260
DB 1201 AGTCTGAGGCTGAGAGCAGTCAAGTGAATTCGCTGAGGCTGAGTGAATCTCTA 1260
QY 1261 GCCCTGTTTGGCTCTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

Db	1261	GCCCTGGTTTTTGGCCTCCTTTTGTGTGCTACACAGCGTGGGTTCTTGTGCAGATGGA	1320
Qy	1321	AGCGACGACAGAGGGGGAACCAAGGGGGTGTGACTACCGCCACGACAGAGTATGCCGAG	1380
Db	1321	AGGCAAGCACAGAGGGGGAACCAAGGGGGTGTGACTACCGCCACGACAGAGTATGCCGAG	1380
Qy	1381	ACTGAGGCGTGAAGCGTCGATCTTGGAGATGTGTGAAGCCAGACGAGGCGATCTGAGGG	1440
Db	1381	ACTGAGGCGTGAAGCGTCGATCTTGGAGATGTGTGAAGCCAGACGAGGCGATCTGAGGG	1440
Qy	1441	GGAGCCGGTAACTGTCTGTCTGTCTCAATTATGCACTTCTTTTAACTGCGCAGAATTT	1500
Db	1441	GGAGCCGGTAACTGTCTGTCTGTCTCAATTATGCACTTCTTTTAACTGCGCAGAATTT	1500
Qy	1501	TTTTTAAATTAATTTTATAAT	1522
Db	1501	TTTTTAAATTAATTTTATAAT	1522

RESULT 6

Sequence 1, Application US/08487077A
Patent No. 6069242

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYTHETICAL: NO
ANTI-SENSE: NO
IS-08-487-077A-1

Query Match	100.0%;	Score 1522;	DB 3;	Length 1522;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1522;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

QY	61	CTGTGTCAAGGCTCACTGTGCAACTGTGTGCTGACCTGTGCTTCTGATGCTGTCCAT	120
Db	61	CTGTGTCAAGGCTCACTGTGCAACTGTGTGCTGACCTGTGCTTCTGATGCTGTCCAT	120
QY	121	CCCCAGAGTGTGCCCGGATGACAGAGATTCCTCCCTTGTGGAGAGAGCTCTTCTTGAGGAA	180
Db	121	CCCCAGAGTGTGCCCGGATGACAGAGATTCCTCCCTTGTGGAGAGAGCTCTTCTTGAGGAA	180
QY	181	GATGACCCACTGTGGCGAGAGAGATCTGTGCCACTGTAAGAGATTACCCAGAGAGAGAT	240
Db	181	GATGACCCACTGTGGCGAGAGAGATCTGTGCCACTGTAAGAGATTACCCAGAGAGAGAT	240
QY	241	CCACCCGGAGAGAGATCTTACTGTGAGAGAGATCTACTGTGAGAGAGATCTTACT	300
Db	241	CCACCCGGAGAGAGATCTTACTGTGAGAGAGATCTACTGTGAGAGAGATCTTACT	300
QY	301	GAAGTTAAGCTTAATCAGAGAGAGGCTCCTGAAATTAGAGATCTTACTTGT	360
Db	301	GAAGTTAAGCTTAATCAGAGAGAGGCTCCTGAAATTAGAGATCTTACTTGT	360
QY	361	GAGGCTCTTGAGATTCCTCAAGAAACCCCAAGATATGCCCCAAGAGACAAAGAGGGAT	420
Db	361	GAGGCTCTTGAGATTCCTCAAGAAACCCCAAGATATGCCCCAAGAGACAAAGAGGGAT	420
QY	421	GACCAAGATCTTGGCGTATGAGAGCGACCCGCGCTTGCCCGGGTGTCCCAAGCTGC	480
Db	421	GACCAAGATCTTGGCGTATGAGAGCGACCCGCGCTTGCCCGGGTGTCCCAAGCTGC	480
QY	481	GGGGGGCGCTTCCAGTCCCCGGTGGATATCCGGCCCCAGCTGCGCGCTTGTGCGCGGC	540
Db	481	GGGGGGCGCTTCCAGTCCCCGGTGGATATCCGGCCCCAGCTGCGCGCTTGTGCGCGGC	540
QY	541	CTGGGCCCCCTGAAACTCTGGGCTTCCAGCTCCGCGCGCTCCAGAACTCGCTGGCG	600
Db	541	CTGGGCCCCCTGAAACTCTGGGCTTCCAGCTCCGCGCGCTCCAGAACTCGCTGGCG	600
QY	601	AACATGAGCCACAGTGTGCAACTGACCTGTCTCTGGGCTTAAAGATGCTTGGGTCC	660
Db	601	AACATGAGCCACAGTGTGCAACTGACCTGTCTCTGGGCTTAAAGATGCTTGGGTCC	660
QY	661	GGGGGGGAGTACCGGGGCTCTGCACTGATCTGCACTGGGGGGCTGCAAGTGTGTCGGGC	720
Db	661	GGGGGGGAGTACCGGGGCTCTGCACTGATCTGCACTGGGGGGCTGCAAGTGTGTCGGGC	720
QY	721	TCGAGACACTGTGAGAGGCACTGTTCCCTGCCAGATCCAAGTGTGTTCACTCAAC	780
Db	721	TCGAGACACTGTGAGAGGCACTGTTCCCTGCCAGATCCAAGTGTGTTCACTCAAC	780
QY	781	ACCGCTTTTGTCAAGATTGACGAGGCTTGGGGCGCCCGGGAGGCTGAGCGTGTGGCC	840
Db	781	ACCGCTTTTGTCAAGATTGACGAGGCTTGGGGCGCCCGGGAGGCTGAGCGTGTGGCC	840
QY	841	GCTTTTCTGAGAGAGGGCCCGGAGAAACAAGTCTATGAGCACTTGTCTGTGCTTG	900
Db	841	GCTTTTCTGAGAGAGGGCCCGGAGAAACAAGTCTATGAGCACTTGTCTGTGCTTG	900
QY	901	GAAGAAATCGCTAGAGAGGCTCAGAGCTCAGGTTCCAGGACTGGAATATCTGCACTC	960
Db	901	GAAGAAATCGCTAGAGAGGCTCAGAGCTCAGGTTCCAGGACTGGAATATCTGCACTC	960
QY	961	CTGGCCCTCTGACTTCAACCGCTATTTCATATAGAGGGTCTCTGACTACACGCGCTGT	1020
Db	961	CTGGCCCTCTGACTTCAACCGCTATTTCATATAGAGGGTCTCTGACTACACGCGCTGT	1020
QY	1021	GCCCAAGGATGCTGCTGACTGTGTTTAAACAGACAGTATGCTGAGTGTCAAGACTC	1080
Db	1021	GCCCAAGGATGCTGCTGACTGTGTTTAAACAGACAGTATGCTGAGTGTCAAGACTC	1080
QY	1081	CACACCTCTCTGACACCTCTGTGGGACCTGTGTACTCTGTGGCTACAGCTGAATCTTCCGA	1140
Db	1081	CACACCTCTCTGACACCTCTGTGGGACCTGTGTACTCTGTGGCTACAGCTGAATCTTCCGA	1140
QY	1140	CACACCTCTCTGACACCTCTGTGGGACCTGTGTACTCTGTGGCTACAGCTGAATCTTCCGA	1200
Db	1140	CACACCTCTCTGACACCTCTGTGGGACCTGTGTACTCTGTGGCTACAGCTGAATCTTCCGA	1200

Db
1081 CACACCCCTCTCTACACACCCCTGTGGGAGACTTGGTGACTTCGGGTACACGCTGAACCTTCCGA 1140

Oy	1141	GCAGACAGCCTTTGAAATGGGCGAGTGAATTAGAGCCTCTTCCCTGCTGAGAGTGAACAGC	1200
Db	1141	GCAGACAGCCTTTGAAATGGGCGAGTGAATTAGAGCCTCTTCCCTGCTGAGAGTGAACAGC	1200
Oy	1201	AGTCCTCGGAGCTGCTGAGCCAGTCCAGCTGAATTCCTGCGCTGCTGATCATTCTTA	1260
Db	1201	AGTCCTCGGAGCTGCTGAGCCAGTCCAGCTGAATTCCTGCGCTGCTGATCATTCTTA	1260
Oy	1261	GCCTCTGCTTTTTCGCTCTCTTTTTCCTGCTCACAGCGTCGGGCTTCTTGTGCAATGAGA	1320
Db	1261	GCCTCTGCTTTTTCGCTCTCTTTTTCCTGCTCACAGCGTCGGGCTTCTTGTGCAATGAGA	1320
Oy	1321	AGGCAGCACAGAAAGGGGAAACCAAAAGGGGGTGTAGACTACCGCCGACAGAGTGTGCCAG	1380
Db	1321	AGGCAGCACAGAAAGGGGAAACCAAAAGGGGGTGTAGACTACCGCCGACAGAGTGTGCCAG	1380
Oy	1381	ACTGAGGCTTGAAGGCTGGAATCTTGAGAAATGTGAGAACCCAGCCAGAGGCAATCTGAGGG	1440
Db	1381	ACTGAGGCTTGAAGGCTGGAATCTTGAGAAATGTGAGAACCCAGCCAGAGGCAATCTGAGGG	1440
Oy	1441	GGAGCCGGTAATCTGTCTCTGTCTCTCATTTATGCACTTCTTTAACTGCGCAAGAAATT	1500
Db	1441	GGAGCCGGTAATCTGTCTCTGTCTCTCATTTATGCACTTCTTTAACTGCGCAAGAAATT	1500
Oy	1501	TTTTAAATTAATAATTATTAAT	1522
Db	1501	TTTTAAATTAATAATTATTAAT	1522

RESULT 7
US-08-485-863A-1

? Sequence 1, Application US/08485863A
? Patent No. 6093548
?
? GENERAL INFORMATION:
? APPLICANT: Zavada, Jan
? APPLICANT: Pastorekova, Silvia
? APPLICANT: Pastorek, Jaromir
? TITLE OF INVENTION: NM Gene and Protein
? NUMBER OF SEQUENCES: 86
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Leona L. Lauder
? STREET: 6 Mariposa Court
? CITY: Tiburon
? STATE: California
? COUNTRY: USA
? ZIP: 94920
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/485,863A
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/260,190
? FILING DATE: 15-JUN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Lauder, Leona L.
? REGISTRATION NUMBER: 30,863
? REFERENCE/DOCKET NUMBER: D-0021.3G
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-435-2034
? TELEFAX: 415-435-0727
?
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1522 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEetical: NO
?

ANTI-SENSE: NO
; US-08-485-863A-1

Query Match	100.0%	Score 1522;	DB 3;	Length 1522;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1522; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

OY	1	ACAGTACAGCGCAATGAGCTCCCTGTGCCCCAGGCCCTGAGCTCCCTGTGTATCCCGACC	60
Db	1	ACAGTACAGCGCAATGAGCTCCCTGTGCCCCAGGCCCTGAGCTCCCTGTGTATCCCGACC	60
OY	61	CTGCTCCAGGCTCACTGTGCAACTGTGCTGTCACTGCTGTTCGATGCTGTCCAT	120
Db	61	CTGCTCCAGGCTCACTGTGCAACTGTGCTGTCACTGCTGTTCGATGCTGTCCAT	120
OY	121	CCCCAGAGGTGTGCCCCGGATGCAAGAGGATTTCCCCCTTGGGAGGAGGCTCTTGGGGAA	180
Db	121	CCCCAGAGGTGTGCCCCGGATGCAAGAGGATTTCCCCCTTGGGAGGAGGCTCTTGGGGAA	180
OY	181	GATGACCCACTGTGGCGAGAGGATCTGCCCACTGAAAGGATTCACCCAGAGAGAGGAT	240
Db	181	GATGACCCACTGTGGCGAGAGGATCTGCCCACTGAAAGGATTCACCCAGAGAGAGGAT	240
OY	241	CCACCCGAGAGAGGATCTAACCCTGAGAGGAGATCTAACCCTGAGAGAGGAGATCTAACC	300
Db	241	CCACCCGAGAGAGGATCTAACCCTGAGAGGAGATCTAACCCTGAGAGAGGAGATCTAACC	300
OY	301	GAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAAGTCTACTTGT	360
Db	301	GAGTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAAGTCTACTTGT	360
OY	361	GAGGCTCTTGAGATCTTCAAGAACCCCAAGATATGCCACAGGACAAAGAGGGAT	420
Db	361	GAGGCTCTTGAGATCTTCAAGAACCCCAAGATATGCCACAGGACAAAGAGGGAT	420
OY	421	GACCAAGATCTTGGGCGTATGAGGGGACCCGGCGCTGGGCCCGGGGTGTCCCAAGCTGC	480
Db	421	GACCAAGATCTTGGGCGTATGAGGGGACCCGGCGCTGGGCCCGGGGTGTCCCAAGCTGC	480
OY	481	GCGGCGCGCTTCCAGTCCCGGTGATATCCGCCCAAGCTCGCGCTTCTGCCCCGGCC	540
Db	481	GCGGCGCGCTTCCAGTCCCGGTGATATCCGCCCAAGCTCGCGCTTCTGCCCCGGCC	540
OY	541	CTGGGCCCCCTGGAACTCTCGGGTTCCAGTCCCGCGCTCCAGAACTGCGCTTGCGC	600
Db	541	CTGGGCCCCCTGGAACTCTCGGGTTCCAGTCCCGCGCTCCAGAACTGCGCTTGCGC	600
OY	601	AACATAGGCAAGATGTGCAACTGACCTGCGCTCTGGGCTAAGATAGGCTCTGGATCCC	660
Db	601	AACATAGGCAAGATGTGCAACTGACCTGCGCTCTGGGCTAAGATAGGCTCTGGATCCC	660
OY	661	GGGCGGGAATACCGGGCTCTGCACTGCACTGAGTGGGGGCTGCAAGTGTCTCGGCG	720
Db	661	GGGCGGGAATACCGGGCTCTGCACTGCACTGAGTGGGGGCTGCAAGTGTCTCGGCG	720
OY	721	TGGAGACACTGTGGAAGGCAACGTTTCCCTGCGAGATCAACGATGTCACTCAAGC	780
Db	721	TGGAGACACTGTGGAAGGCAACGTTTCCCTGCGAGATCAACGATGTCACTCAAGC	780
OY	781	ACCGCTTTGCGAAGTTGACGAGGCTTTGGGGCGCCCGGAGGCTTGCGGTTGGCC	840
Db	781	ACCGCTTTGCGAAGTTGACGAGGCTTTGGGGCGCCCGGAGGCTTGCGGTTGGCC	840
OY	841	GCTTTTCTGAGAGAGGGCCCGGAAGAAACAGTGCCTATAGCAGTGTGTCTCTCGCTG	900
Db	841	GCTTTTCTGAGAGAGGGCCCGGAAGAAACAGTGCCTATAGCAGTGTGTCTCTCGCTG	900
OY	901	GAGAAATGCTGAGAGAGGCTCAGAGCTCAGAGTCCAGGACTTCCAGACTGTGACATATCTGCACTC	960
Db	901	GAGAAATGCTGAGAGAGGCTCAGAGCTCAGAGTCCAGGACTTCCAGACTGTGACATATCTGCACTC	960
OY	961	CTGCTCTTCACTTCAAGCGCTACTTCCAAATATGAGGGGTCTGTACTACACCGGCTGT	1020

Db 961 CTGCCCTGACTGACCGGCTACTTCCAAATATGAGGGGCTCTGTGACTACCGCCCTGT 1020
QY 1021 GCCCAGGGGTGATCTGGACTGTGTTAAACGACAGATGCTGAGTCTAAGCAGCTC 1080
Db 1021 GCCCAGGGGTGATCTGGACTGTGTTAAACGACAGATGCTGAGTCTAAGCAGCTC 1080
QY 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGATCTCTGCTAAGCTGAATCTCCGA 1140
Db 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGATCTCTGCTAAGCTGAATCTCCGA 1140
QY 1141 GCGAGCGACCTTTTGAATGAGGCGAGTGAATTGAGGCTCTCTCTGCTGAGTGAAGC 1200
Db 1141 GCGAGCGACCTTTTGAATGAGGCGAGTGAATTGAGGCTCTCTCTGCTGAGTGAAGC 1200
QY 1201 AGTCCCTGGGCTGTGAGCGACGTCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGA 1260
Db 1201 AGTCCCTGGGCTGTGAGCGACGTCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGA 1260
QY 1261 GCCCTGTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1261 GCCCTGTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 AGGCGACACAGAAAGGGGAAACAAAGGGGGTGTGAGCTACCGCCGACAGAGTGAAG 1380
Db 1321 AGGCGACACAGAAAGGGGAAACAAAGGGGGTGTGAGCTACCGCCGACAGAGTGAAG 1380
QY 1381 ACTGAGCTTAAGAGCTGATCTTGAAGATGTGAAGAACCGCCGACAGAGTGAAGG 1440
Db 1381 ACTGAGCTTAAGAGCTGATCTTGAAGATGTGAAGAACCGCCGACAGAGTGAAGG 1440
QY 1441 GGAGCGGTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
Db 1441 GGAGCGGTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
QY 1501 TTTTAAATTAATTAATTAAT 1522
Db 1501 TTTTAAATTAATTAATTAAT 1522

RESULT 8
US-08-485-049D-1
Sequence 1, Application US/08485049D
Patent No. 6204370
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
US-08-485-049D-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGAGCTCCCTGTGAGCCCGCCCTGCTCTGTGATCCCGGC 60
Db 1 ACAGTCAGCCGATGAGCTCCCTGTGAGCCCGCCCTGCTCTGTGATCCCGGC 60
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Db 61 CCTGCTCCAGGCTCTCACTGTGCACTGTCTGTCTCACTGTCTGTGATGCTGCT 120
QY 121 CCCGAGGTTGCCCGGATGCAAGAGATTCCTCTGAGGAGGCTCTTCTGGGGA 180
Db 121 CCCGAGGTTGCCCGGATGCAAGAGATTCCTCTGAGGAGGCTCTTCTGGGGA 180
QY 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAT 240
Db 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAT 240
QY 241 CCAACCGGAGAGAGATTTACTTGAAGAGATTTACTTGAAGAGAGATTTACTT 300
Db 241 CCAACCGGAGAGAGATTTACTTGAAGAGATTTACTTGAAGAGAGATTTACTT 300
QY 241 CCAACCGGAGAGAGATTTACTTGAAGAGATTTACTTGAAGAGAGATTTACTT 300
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Db 421 GACAGAGTCATTGGGCTATGAGGCGACCCGCTGAGGCTGAGGCTGAGGCTG 480
QY 481 GGGGCGGCTTCAATCCCGGTTGATTCGCGCCCGCCAGCTGCGGCTTTCGCGCG 540
Db 481 GGGGCGGCTTCAATCCCGGTTGATTCGCGCCCGCCAGCTGCGGCTTTCGCGCG 540
QY 541 CTGCGCCCTGAACTCTGAGGCTTCCAGCTCCGCGCTCCAGAACTGAGGCTGCG 600
Db 541 CTGCGCCCTGAACTCTGAGGCTTCCAGCTCCGCGCTCCAGAACTGAGGCTGCG 600
QY 601 AACATGCGCAAGTGTGCACTGACCTGCTCTGAGGCTGAGGCTGAGGCTGAG 660
Db 601 AACATGCGCAAGTGTGCACTGACCTGCTCTGAGGCTGAGGCTGAGGCTGAG 660
QY 661 GGGCGGAGTACCGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
Db 661 GGGCGGAGTACCGGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
QY 721 TCGAGACACTGTGGAAGGCAACGCTTCTCTGCGAGATCAAGTGTGCTCAAG 780
Db 721 TCGAGACACTGTGGAAGGCAACGCTTCTCTGCGAGATCAAGTGTGCTCAAG 780
QY 781 ACCGCTTTGCAAGTTGACAGAGGCTTGGGCGCGCGGAGGCTGAGGCTGAG 840
Db 781 ACCGCTTTGCAAGTTGACAGAGGCTTGGGCGCGCGGAGGCTGAGGCTGAG 840

Qy	841	GCCTTTCGAGAGGAGGCGCCGGAGAAAA	CAGTGCCTTAATGAGCAGTTCGTGCTG	900
Db	841	GCTTTCGAGAGAGGCGCCGGAGAAAA	CAGTGCCTTAATGAGCAGTTCGTGCTG	900
Qy	901	GAAAGAAATCGCTGAGAGAAAGGCTC	CAGAGACTCAGGTC	960
Db	901	GAAAGAAATCGCTGAGAGAAAGGCTC	CAGAGACTCAGGTC	960
Qy	961	CTGCGCCTCTGACTTTCAGGCGCGCT	CAATTAATGAGGGGTCTCTGACTAACCCGCGCTG	1022
Db	961	CTGCGCCTCTGACTTTCAGGCGCGCT	CAATTAATGAGGGGTCTCTGACTAACCCGCGCTG	1022
Qy	1021	GCCCAAGGAGTGCATCTGAGCTGTGTTTAA	CCAGACAGTAGTACTGAGTCAAGCAGCTC	1082
Db	1021	GCCCAAGGAGTGCATCTGAGCTGTGTTTAA	CCAGACAGTAGTACTGAGTCAAGCAGCTC	1082
Qy	1081	CACACCCCTCTCTGACACACCTGTGGGGA	CTGGTACTCTCGGCTACAGCTGAATCTTCCGA	1140
Db	1081	CACACCCCTCTCTGACACACCTGTGGGGA	CTGGTACTCTCGGCTACAGCTGAATCTTCCGA	1140
Qy	1141	GCGACGACGACCTTTGAATGGGCGAGTGA	ATTGAGGCGCTCCTTCCCTGCTGAGTGGACAGC	1200
Db	1141	GCGACGACGACCTTTGAATGGGCGAGTGA	ATTGAGGCGCTCCTTCCCTGCTGAGTGGACAGC	1200
Qy	1201	AGTCTCGGAGCTGCTGAGCCAGTCCAGCTGA	ATTCTGCGCTGGCTGCTGGTGAATCTCTA	1260
Db	1201	AGTCTCGGAGCTGCTGAGCCAGTCCAGCTGA	ATTCTGCGCTGGCTGCTGGTGAATCTCTA	1260
Qy	1261	GCCCTCGATTTTGGCTCCTCTTTTGGCTG	CTGCACCAAGCGCGGTTCCCTGTGCAATGAGA	1320
Db	1261	GCCCTCGATTTTGGCTCCTCTTTTGGCTG	CTGCACCAAGCGCGGTTCCCTGTGCAATGAGA	1320
Qy	1321	AGGCAAGCACAAGAGGGGAAACCAAAGGG	GGGTGTGAGCTACCGCCACGACAGAGTACCAG	1380
Db	1321	AGGCAAGCACAAGAGGGGAAACCAAAGGG	GGGTGTGAGCTACCGCCACGACAGAGTACCAG	1380
Qy	1381	ACTGGAGCCTTGAAGGCTGAGATCTTGGAA	AAATGTGAGAACCAAGCCAGAGGCAATCTGAGG	1440
Db	1381	ACTGGAGCCTTGAAGGCTGAGATCTTGGAA	AAATGTGAGAACCAAGCCAGAGGCAATCTGAGG	1440
Qy	1441	GGAGCGGTTAACTGTCTGTCTGCTCATTA	TATGCACTTCCTTTTAACTGCGCAAGAAATT	1500
Db	1441	GGAGCGGTTAACTGTCTGTCTGCTCATTA	TATGCACTTCCTTTTAACTGCGCAAGAAATT	1500
Qy	1501	TTTTTAAATTAATATTTTAAAT	1522	
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RESULT 9
US-09-178-115-1

/ Sequence 11, Application US/09178115

/ Patent No. 6297041

/ GENERAL INFORMATION:

/ APPLICANT: Zavada, Jan

/ APPLICANT: Pastorekova, Silvia

/ APPLICANT: Pastorek, Jaromir

/ TITLE OF INVENTION: MN Gene and Protein

/ FILE REFERENCE: D-0021_5A

/ CURRENT APPLICATION NUMBER: US/09/178,115

/ CURRENT FILING DATE: 1998-10-23

/ EARLIER APPLICATION NUMBER: 09/177,776

/ EARLIER FILING DATE: 1998-10-23

/ EARLIER APPLICATION NUMBER: 08/787,739

/ EARLIER FILING DATE: 1997-01-24

/ EARLIER APPLICATION NUMBER: 08/485,049

/ EARLIER FILING DATE: 1995-06-07

/ EARLIER APPLICATION NUMBER: 08/486,756

/ EARLIER FILING DATE: 1995-06-07

/ EARLIER APPLICATION NUMBER: 08/477,504

/ EARLIER FILING DATE: 1995-06-07

/ EARLIER APPLICATION NUMBER: 08/481,658

/ EARLIER FILING DATE: 1995-06-07

	Query Match	100.0%	Score 1522;	DB 3;	Length 1522;
	Best Local Similarity	100.0%	Pred. No. 0;		
	Matches 1522;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0
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1	ACAGTCAGCCGCATAGGCTCCCTGTGCCCCAGCCCTGGCTCCCTGTGTATCCCGGCC				
61	CTGTGTCAGGCTCTCATCTGTGCAACTGTGCTGTCTCATCTGTGCTTGTATGCTGTCCAT				
61	CTGTGTCAGGCTCTCATCTGTGCAACTGTGCTGTCTCATCTGTGCTTGTATGCTGTCCAT				
121	CCCCAGAGGTGGCCCCCGGATGCAAGAGGATCCCCCTTGGAGAGAGGCTCTTGGGGGA				
121	CCCCAGAGGTGGCCCCCGGATGCAAGAGGATCCCCCTTGGAGAGAGGCTCTTGGGGGA				
121	CCCCAGAGGTGGCCCCCGGATGCAAGAGGATCCCCCTTGGAGAGAGGCTCTTGGGGGA				
181	GATGACCCCATCTGGCGAGAGAGATCTGCCCCAGTGAAGAGATTCCACCCAGAGAGAGAT				
181	GATGACCCCATCTGGCGAGAGAGATCTGCCCCAGTGAAGAGATTCCACCCAGAGAGAGAT				
241	CCACCCCGAGAGAGATCTACCTGTGAGAGAGGATCTACCTGGAGAGAGAGATTACT				
241	CCACCCCGAGAGAGATCTACCTGTGAGAGAGGATCTACCTGGAGAGAGAGATTACT				
301	GAGTTAAGCTTAATAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACTTACT				
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361	GAGCTCTCTGAGATCTCTCAAGAACCCCAAGATTATGCCCAAGAGGAGGAGAT				
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421	GACACGAGTCAATTGGCGCTAATGAGAGGCAACCGCGCTAGCCCGGAGTGTCCCAAGCTGCG				
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481	GCGGAGCGCTTCAAGTCCCGGAGATATCCGCCCAAGCTGCGCTTCTGCGCGGCC				
481	GCGGAGCGCTTCAAGTCCCGGAGATATCCGCCCAAGCTGCGCTTCTGCGCGGCC				
541	CTGGGCCCCCTGGAATCTCCGGGCTTCCAGTCTCCGCGCTTCCAGAACTGCGCTGCGC				
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601	AACAAATGAGCAAGTGTGCAACTGACCTGCTCTGAGGCTAAGAGATGGCTCTGGATCCC				
601	AACAAATGAGCAAGTGTGCAACTGACCTGCTCTGAGGCTAAGAGATGGCTCTGGATCCC				

Db	601	AAACAATGGCCACACAGTGTGCAATGACACCTTCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC	660
Oy	661	GGGCGGGAAGTACCGGGCTCTGCACTGCAATCTGCACTGCGGGGCTGCAAGGTCTGCGGGC	720
Db	661	GGGCGGGAAGTACCGGGCTCTGCAAGCTGCAATCTGCACTGCGGGGCTGCAAGGTCTGCGGGC	720
Oy	721	TGGAGGCAACATGTGGAAAGGCCACCGCTTTCCTGCGCGAATTCACGTGGTTCACCTCAGC	780
Db	721	TGGAGGCAACATGTGGAAAGGCCACCGCTTTCCTGCGCGAATTCACGTGGTTCACCTCAGC	780
Oy	781	ACCGGCTTTCGACAGATTACGAGGGCTTGGGGGCGCCGGGAGGCGCTGGCGGTGGGC	840
Db	781	ACCGGCTTTCGACAGATTACGAGGGCTTGGGGGCGCCGGGAGGCGCTGGCGGTGGGC	840
Oy	841	GCCCTTTCGAGAGGGGCCCGGAAAGAAAACAGTGCCTATGAGCAGTGTGCTGTCTGCTTG	900
Db	841	GCCCTTTCGAGAGGGGCCCGGAAAGAAAACAGTGCCTATGAGCAGTGTGCTGTCTGCTTG	900
Oy	901	GAAAGAAATGCTGAGGAAAGGCTCAGAGACTCAGGTCCAGAGACTGACATATTCGACTC	960
Db	901	GAAAGAAATGCTGAGGAAAGGCTCAGAGACTCAGGTCCAGAGACTGACATATTCGACTC	960
Oy	961	CTGGCCTCTGACCTTGACCGGCTACTTCGAATGAGGGGCTGTGACTACACCGCCCTGT	1020
Db	961	CTGGCCTCTGACCTTGACCGGCTACTTCGAATGAGGGGCTGTGACTACACCGCCCTGT	1020
Oy	1021	GCCGAGGGTGTCACTGACCTGTGTTTAAACAGACAGTGAATGCTGAGTGTAAAGCAGCTC	1080
Db	1021	GCCGAGGGTGTCACTGACCTGTGTTTAAACAGACAGTGAATGCTGAGTGTAAAGCAGCTC	1080
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Db	1081	CACACCTCTCTGACACCCCTGTGGGGACCTGTGACTCTTGGGCTAACAGCTGAACCTTCCGA	1140
Oy	1141	GCGAGGACGCTTTGAATGGGGAGAGATTGAGGCTCCTTCCCTGCTGAGTGAAGCAGC	1200
Db	1141	GCGAGGACGCTTTGAATGGGGAGAGATTGAGGCTCCTTCCCTGCTGAGTGAAGCAGC	1200
Oy	1201	AGTCTCGGGCTGCTGAGCAGTCCAGCTGAATCTCTGCTGGCTGCTGAGTGAATCTCTTA	1260
Db	1201	AGTCTCGGGCTGCTGAGCAGTCCAGCTGAATCTCTGCTGGCTGCTGAGTGAATCTCTTA	1260
Oy	1261	GCCCTGTGTTTGGGCTCCTTTTTCGTGCAACAGCGTGGCGTTCTTGTGCAAGATGAGA	1320
Db	1261	GCCCTGTGTTTGGGCTCCTTTTTCGTGCAACAGCGTGGCGTTCTTGTGCAAGATGAGA	1320
Oy	1321	AGGCAACACAGAAAGGGGAAACAAAGGGGGTGGAGCTAACCGCCACACAGATGAGCCGAG	1380
Db	1321	AGGCAACACAGAAAGGGGAAACAAAGGGGGTGGAGCTAACCGCCACACAGATGAGCCGAG	1380
Oy	1381	ACTGAGCCTTAGAGGCTGTGATCTTGGAGATGGAAGACACAGCCAGAGGCACTTGAGGG	1440
Db	1381	ACTGAGCCTTAGAGGCTGTGATCTTGGAGATGGAAGACACAGCCAGAGGCACTTGAGGG	1440
Oy	1441	GGAGCGGTAACGTGCTCTGTCTGCTCAATTATGCCACTTCTTTTAACTGCGCAAGAAAT	1500
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RESULT 10

US-09-177-776-1

Sequence 1, Application US/09177776A

Patent No. 6297051

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

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? FILE REFERENCE: D-0021.5A
? CURRENT APPLICATION NUMBER: US/09/177,776A
? CURRENT FILING DATE: 1998-10-23
? EARLIER APPLICATION NUMBER: 08/787,739
? EARLIER FILING DATE: 1997-01-24
? EARLIER APPLICATION NUMBER: 08/485,049
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/486,756
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/477,504
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/481,658
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/485,862
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/485,863
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/487,077
? EARLIER FILING DATE: 1995-06-07
? EARLIER APPLICATION NUMBER: 08/260,190
? EARLIER FILING DATE: 1994-06-15
? EARLIER APPLICATION NUMBER: 08/177,093
? EARLIER FILING DATE: 1993-12-30
? EARLIER APPLICATION NUMBER: 07/964,589
? EARLIER FILING DATE: 1992-10-21
? EARLIER APPLICATION NUMBER: PV-709-92
? EARLIER FILING DATE: 1992-03-11
? NUMBER OF SEQ ID NOS: 116
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
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? ORGANISM: HUMAN
? FEATURE:
? NAME/KEY: CDS
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? FEATURE:
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? LOCATION: (124)..(1389)
US-09-177-776-1

Query Match      100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61   CTGCTCCAGGCTCACTGTGCAACTGTCTGTCACTGTCTGTCTGTGATCCGTGCAT    120
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QY     121   CCCCAAGAGTTGCCCGCCGATGACAGAGATTCCCCTTTGGAGAAGAGCTCTTCTGGGAA    180
DB     121   CCCCAAGAGTTGCCCGCCGATGACAGAGATTCCCCTTTGGAGAAGAGCTCTTCTGGGAA    180

QY     121   GATGACCACACTGGCGAGAGATCTGCGCCAGTAAGAGATTACCCAGAGAGAGAT    240
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QY     181   CCACCCGGAAGAGAGATCTAACCTTGAGAGAGAGATCTACTGTGAGAGAGATCTACT    300
DB     241   CCACCCGGAAGAGAGATCTAACCTTGAGAGAGAGATCTACTGTGAGAGAGATCTACT    300

QY     301   GAAGTTAAGCTTAATAATCAAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAACCTGT    360
DB     301   GAAGTTAAGCTTAATAATCAAGAAAGAGAGGCTCCCTGAAGTTAAGAGATCTAACCTGT    360

QY     361   GAGGCTCCTGGAGATCTCAAGAACCCCAAGTAATAGCCCAAGGAGCAAAAGAGGGAGT    420
DB     361   GAGGCTCCTGGAGATCTCAAGAACCCCAAGTAATAGCCCAAGGAGCAAAAGAGGGAGT    420

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Db 1501 TTTTAAATTAATTAATTAAT 1522

RESULT 11
US-09-772-719B-1
Sequence 1, Application US/09772719B
Patent No. 6770438
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
Pastorek, Jarmir
Pastorekova, Silvia
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 465 California Street, Suite 450
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,719B
FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30, 863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-772-719B-1

Query Match 100.0%; Score 1522; DB 4; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACACTCAGCCGACAGTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
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Db 121 CCCAGAGTTGCCCGGATGCAAGAGATTTCCCTTGGAGAGGCTCTTCTGGGAAA 180
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Db 181 GATGACCACTGGGCGAGAGAGATCTGCCAGATGAAGAGATTCACCAGAGAGAGAT 240
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| 241 |GAAAGTAACTTAATCAGAAAGAGGCTCCCTGAAAGTAAAGATCTACTG| 360
| 301 |GAAAGTAACTTAATCAGAAAGAGGCTCCCTGAAAGTAAAGATCTACTG| 360
| 361 |GAGGCTCTGAGAGTCTTCAAGAACCCAGATATATGCCAGAGGGAACAAGAGGAGAT| 420
| 420 |GAGGCTCTGAGAGTCTTCAAGAACCCAGATATATGCCAGAGGGAACAAGAGGAGAT| 420
| 421 |GACCAAGATCATTTGGGCTATGAGAGGGAACCGCCCTGAGCCGGGATGCCAAGCTGG| 480
| 481 |GCGGGCCGCTTCCAGATCTCCCGGATATCCCGCCAGCTCCGCTTCTGCTCCGCGCC| 540
| 541 |CTGGGCCCCCTGGAATCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGGCTGGCC| 600
| 601 |AACCAATGGCCACAGTGTGCAATGACCTGCTCTGAGGCTAAGATGAGCTCTGGGCTCC| 660
| 661 |AACCAATGGCCACAGTGTGCAATGACCTGCTCTGAGGCTAAGATGAGCTCTGGGCTCC| 660
| 661 |GAGGCGGAGATACCGGCTCTGAGCTGATCTGCACTGGGAGGCTGAGGCTCTGGGCTCC| 720
| 721 |TGGGAGACACATGTGAGAGGAGCCGCTTCCCGGAGATCCAGCTGGTTCACCTCAGC| 780
| 781 |TGGGAGACACATGTGAGAGGAGCCGCTTCCCGGAGATCCAGCTGGTTCACCTCAGC| 780
| 781 |ACGCGCTTTGGCAGAGTTGACAGAGGCTTGGGAGGAGGCTTGGGAGGCTTGGGAGGCT| 840
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| 841 |GCTTTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 900
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| 901 |GAAAGAAATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 960
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| 1021 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1080
| 1081 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1080
| 1081 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1140
| 1141 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1140
| 1141 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1200
| 1201 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1200
| 1201 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1260
| 1261 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1320
| 1321 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1380
| 1321 |GCTCCAGGAGTGTCTGAGCTGTGTTAACAGAGAGTGTGAGTGTGAGAGGAGGCTC| 1380

1321 |AGGACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 1380
1381 |ACTGAGGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 1440
1381 |ACTGAGGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 1440
1441 |GAGGCGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG| 1500
1441 |GAGGCGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG| 1500
1501 |TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA| 1522
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RESULT 12
US-08-260-190-5
; Sequence 5, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13) .. (1389)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (124) .. (1389)
US-08-260-190-5

Query Match 100.0%; Score 1522; DB 4; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 |ACAGTACGCGGAGTGTCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 60
1 |ACAGTACGCGGAGTGTCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 60
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61 |CTGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 120
121 |CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 180
121 |CCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 180
181 |GATGACCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG| 240
181 |GATGACCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG| 240
241 |CAACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 300
241 |CAACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 300
301 |GAAAGTAACTTAATCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 360
301 |GAAAGTAACTTAATCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG| 360

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Db 481 AATGGCCACAGTGTGACCTGACCTGCTCCCTGGGCTAGAGATGCTGAGGATCCCGG 540
Qy 664 CGGAGATACCGGCTTGTGACGCTGATCTGCACTGGGGGGCTGCAAGTGTCCGGGCTG 723
Db 541 CGGAGATACCGGCTTGTGACGCTGATCTGCACTGGGGGGCTGCAAGTGTCCGGGCTG 600
Qy 724 GAGCACTGTGGAAGGCAACCGTTCCCTGCGGAGATCAGGTGTTCAACCTCAGCACC 783
Db 601 GAGCACTGTGGAAGGCAACCGTTCCCTGCGGAGATCAGGTGTTCAACCTCAGCACC 660
Qy 784 GCTTTGCGAGATTGACGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTTGGCGCGC 843
Db 661 GCTTTGCGAGATTGACGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTTGGCGCGC 720
Qy 844 TTTCTGAGAGAGGCGCCGAGAGAAAAGTGTCTATGAGCAGTTGCTGTCTGCTTGA 903
Db 721 TTTCTGAGAGAGGCGCCGAGAGAAAAGTGTCTATGAGCAGTTGCTGTCTGCTTGA 780
Qy 904 GAAATGCTGAGGAGGCTCAGAGCTCAGAGTCCCGAGACTGGAATATCTGCACTCCG 963
Db 781 GAAATGCTGAGGAGGCTCAGAGCTCAGAGTCCCGAGACTGGAATATCTGCACTCCG 840
Qy 964 CCTCTGACTTACGCGCTACTTCAATATGAGGGGCTCTGACTACCGCGCTGTGCG 1023
Db 841 CCTCTGACTTACGCGCTACTTCAATATGAGGGGCTCTGACTACCGCGCTGTGCG 900
Qy 1024 CAGGCTGATCTGAGCTGTGTTAACAGACAGTGTGAGTGTGCTAAGCAGCTCCAC 1083
Db 901 CAGGCTGATCTGAGCTGTGTTAACAGACAGTGTGAGTGTGCTAAGCAGCTCCAC 960
Qy 1084 ACCCTCTGAGCAACCTGTGGGGGAGCTGTGAGTCTCCGCTACAGTGAATCTCCAGG 1143
Db 961 ACCCTCTGAGCAACCTGTGGGGGAGCTGTGAGTCTCCGCTACAGTGAATCTCCAGG 1020
Qy 1144 AGCAGACCTTGTGATGGGCGAGTGTGAGGCTCTCTCCCTGCTGAGTGTGAGCAGCAGT 1203
Db 1021 AGCAGACCTTGTGATGGGCGAGTGTGAGGCTCTCTCCCTGCTGAGTGTGAGCAGCAGT 1080
Qy 1204 CCTCGGGCTGTGAGCAGTCCAGTGAATCTCTGCTGGCTGCTGTGATCATCTTACG 1263
Db 1081 CCTCGGGCTGTGAGCAGTCCAGTGAATCTCTGCTGGCTGCTGTGATCATCTTACG 1140
Qy 1264 CTGGTTTGGGCTCTTTTGTGTGACAGAGTGTGGCTCTCTTGTGAGTGAAGAAAG 1323
Db 1141 CTGGTTTGGGCTCTTTTGTGTGACAGAGTGTGGCTCTCTTGTGAGTGAAGAAAG 1200
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Db 1261 GAGGCTTGAAGGCTGTGATTTGAGAAATGTGAGAACCAAGCAGAGCATCTGAGGGGGA 1320
Qy 1444 GCGGCTTGAAGGCTGTGATTTGAGAAATGTGAGAACCAAGCAGAGCATCTGAGGGGGA 1503
Db 1321 GCGGCTTGAAGGCTGTGATTTGAGAAATGTGAGAACCAAGCAGAGCATCTGAGGGGGA 1380
Qy 1504 TAAATTAATTAATTAAT 1522
Db 1381 TAAATTAATTAATTAAT 1399

FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-260-190-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAGAGGTTGCCCGAGATGAGAGGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAGAGAT 60
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Db 61 GACCCACTGGGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGATTCGA 120
Qy 244 CCGGAGAGAGAGATTCCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAA 303
Db 121 CCGGAGAGAGAGATTCCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAA 180
Qy 304 GTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTGAAGATTCATCTACTGTTGAG 363
Db 181 GTTAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTGAAGATTCATCTACTGTTGAG 240
Qy 364 GCTCTGAGAGATTCCTCAAGAACCCCAAGATTAATGCCCAGAGGACAAAGAGGGATGAC 423
Db 241 GCTCTGAGAGATTCCTCAAGAACCCCAAGATTAATGCCCAGAGGACAAAGAGGGATGAC 300
Qy 424 CAGAGTCAATGGCGCTATGAGAGCCAGCCGCTGTGCGCCGCTGCTCCCAAGCTTGGCG 483
Db 301 CAGAGTCAATGGCGCTATGAGAGCCAGCCGCTGTGCGCCGCTGCTCCCAAGCTTGGCG 360
Qy 484 GGCCTTCAGTCCCGGTGATATCCGCGCCCAAGCTGCGGCTTGTGCGCGGCTG 543
Db 361 GGCCTTCAGTCCCGGTGATATCCGCGCCCAAGCTGCGGCTTGTGCGCGGCTG 420
Qy 544 CCGCCCTTGAATCTCTGAGCTTCCAGCTCCGCGCTCCCAAGATCTGCGCTGCGCAAC 603
Db 421 CCGCCCTTGAATCTCTGAGCTTCCAGCTCCGCGCTCCCAAGATCTGCGCTGCGCAAC 480
Qy 604 AATGGCACAGTGTGCACTGACCTGCTCTGAGATGAGATGCTTGGGTCCGGG 663
Db 481 AATGGCACAGTGTGCACTGACCTGCTCTGAGATGAGATGCTTGGGTCCGGG 540
Qy 664 CGGAGTACCGGAGCTGTGAGCTGAGCTTGAAGCTGAGGAGGCTGAGAGTGTCCGGGCTG 723
Db 541 CGGAGTACCGGAGCTGTGAGCTGAGCTTGAAGCTGAGGAGGCTGAGAGTGTCCGGGCTG 600
Qy 724 GAGCACTGTGGAAGGCAACCGTTCCCTGCGGAGATCAGGTGTTCACTCAGCACC 783
Db 601 GAGCACTGTGGAAGGCAACCGTTCCCTGCGGAGATCAGGTGTTCACTCAGCACC 660
Qy 784 GCTTTGCGAGATTGACGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTGTTGGCGCGC 843
Db 661 GCTTTGCGAGATTGACGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTGTTGGCGCGC 720
Qy 844 TTTCTGAGAGAGGCGCCGAGAGAAAAGTGTCTATGAGCAGTTGCTGTGCTGCTTGA 903

Db	721	TTTCTGAGAGAGGAGCCCGAAGAAAACA	GCTTATGAGAGATTGCTGTCTGCTTGGAA	780
Qy	904	GAAATTCGCTGAGAAAGGCTCA	GAGACTCAGGCTCCAGACTGGA	CAATATTCGACTTCCTG 963
Db	781	GAAATTCGCTGAGAAAGGCTCA	GAGACTCAGGCTCCAGACTGGA	CAATATTCGACTTCCTG 840
Qy	964	CCCTCTGACTCAGCCGCTACTTCC	AATATGAGGGGCTCTCTGACTCA	CCGCCCTGTGCG 102
Db	841	CCCTCTGACTCAGCCGCTACTTCC	AATATGAGGGGCTCTCTGACTCA	CCGCCCTGTGCG 900
Qy	1024	CAGGGTGTATCTGCACTGTGTTTAA	CCAGACAGTATGCTGAGTGAAGCA	GCTTCCAC 108
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Qy	1084	ACCCTCTCTGACACCCCTGTGGGGG	ACCTGGGATCTCCGGCTCAGCTGAA	CACTTCCGAGG 114
Db	961	ACCCTCTCTGACACCCCTGTGGGGG	ACCTGGGATCTCCGGCTCAGCTGAA	CACTTCCGAGG 102
Qy	1144	ACGCAGCCCTTGAATGAGGCGAGTAT	TGAGGCTCTCTTCCCTGCTGAGTGA	CAGCAAGT 120
Db	1021	ACGCAGCCCTTGAATGAGGCGAGTAT	TGAGGCTCTCTTCCCTGCTGAGTGA	CAGCAAGT 108
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Db	1081	CCTGGGGCTGCTGAGCGCAATCC	AGCTGAATTCCTGCTGGCTGCTGTGA	CAATCTTACGC 114
Qy	1264	CTGTGTTTGGGCTCTCTTTTCTGTG	CACACAGCGTGCAGCTTCTTGTGCA	GATGAGAAAG 132
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Qy	1334	CAGCAACAGAAAGGGAAACCAA	AGGGGCTGTGAGCTACGCCCAGCA	GAGTGAAGCGAGACT 138
Db	1201	CAGCAACAGAAAGGGAAACCAA	AGGGGCTGTGAGCTACGCCCAGCA	GAGTGAAGCGAGACT 126
Qy	1384	GGAGGCTAGAGGCTGGATCTT	GAGAAATGGAAGACCAAGCAGAG	GCATCTGAGGGGGA 144
Db	1281	GGAGGCTAGAGGCTGGATCTT	GAGAAATGGAAGACCAAGCAGAG	GCATCTGAGGGGGA 132
Qy	1444	GCCGGTAACGTGCTGCTGCTCAT	TATGCACTTCTTTTAACTGCCA	AGAAATTTTT 150
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; Sequence 1, Application US/07964589				
; Patent No. 5387676				
; GENERAL INFORMATION:				
; APPLICANT: Zavada, Jan				
; APPLICANT: Pastorekova, Silvia				
; APPLICANT: Pastorek, Jaromir				
; TITLE OF INVENTION: MN Gene and Protein				
; NUMBER OF SEQUENCES: 4				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Leona L. Lauder				
; STREET: Steuart Street Tower, 18th Fl., One Market				
; CITY: Plaza				
; STATE: San Francisco				
; COUNTRY: USA				
; ZIP: 94105				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Floppy disk				
; COMPUTER: IBM PC compatible				
; OPERATING SYSTEM: PC-DOS/MS-DOS				
; SOFTWARE: PatentIn Release #1.0, Version #1.25				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/07/964.589				

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? FILING DATE: 19921021
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Lauder, Leona L
? REGISTRATION NUMBER: 30,863
? REFERENCE/DOCKET NUMBER: D-0021
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-777-9257
? TELEFAX: 415-543-4219
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1397 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEITICAL: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1287
?
US-07-964-589-1

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Query Match	34.7%;	Score 528;	DB 1;	Length 1397;	
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Qy	935	TCCCAAGACATGGAATATATTGCAATCTCTGCGCCCTCTGACTTCAAGCCGCTACTTCCAAATAG	994		
Db	809	TTCCAGAGACTGGAATATATTGCACTCTCTGCGCCCTCTGACTTCAAGCCGCTACTTCCAAATAG	868		
Qy	995	AGGGGTCTGTGACTACACCGCCCTGTGCCCGGAGGTGCATCTGACATGTGTTAAACAGA	1054		
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Qy	1055	CAGTATGATGTAAGTGTCTAAGCAAGTCCAACACCTCTCTGACACCCCTGTGGGACCTGGTG	1114		
Db	929	CAGTATGATGTAAGTGTCTAAGCAAGTCCAACCTCTCTGACACCCCTGTGGGACCTGGTG	988		
Qy	1115	ACTCTGGGCTACAGCTGAACCTTCCGAGCGACCGACCTTTGAATGGGGGAGTGAATTGAG	1177		
Db	989	ACTCTGGGCTACAGCTGAACCTTCCGAGCGACCGACCTTTGAATGGGGGAGTGAATTGAG	1044		
Qy	1175	CCTCCTTCCCTGTGAGTGGACAGCAGTCTCTGGGCTGTGAGCCAGTCCAGCTGAATT	1234		
Db	1049	CCTCCTTCCCTGTGAGTGGACAGCAGTCTCTGGGCTGTGAGCCAGTCCAGCTGAATT	1108		
Qy	1235	CTGTCCCTGGCTGTGTGTGACATCTTACCCCTGGTTTTTGGGCTCTCTTTTGTGTCTACCA	1299		
Db	1109	CTGTCCCTGGCTGTGTGTGACATCTTACCCCTGGTTTTTGGGCTCTCTTTTGTGTCTACCA	1166		
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Qy	1355	GC-TACCGCCCAAGCAGAGGTAGCCGAGACTTGAGGCTTGAAGCTTGATCTTTGAGAAATGT	1413		
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Qy	1414	GAGAAAGCAACCGAGGCACTGAGAGGGGGAGCCGGTGAACCTGTCCGTGCTCCTCAATATAG	1473		
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Job time : 158 secs

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TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-772-719-1

Query Match 100.0%; Score 1522; DB 9; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTAGCGGATGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCC 60
DB 1 ACAGTAGCGGATGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCC 60
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QY 181 GATGACCCACTGGGCGAGAGAGATCTGCGCAGTGAAGAGATTTCAACCCAGAGAGAGAT 240
DB 181 GATGACCCACTGGGCGAGAGAGATCTGCGCAGTGAAGAGATTTCAACCCAGAGAGAGAT 240
QY 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
QY 301 GAAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATTTACTTACTGTT 360
DB 301 GAAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATTTACTTACTGTT 360
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DB 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAATGCCACAGAGAGAGAGAT 420
QY 421 GACCAAGATCATTTGGGCTATGAGAGGCAACCGCCCTGGCCCGGGGTGTCCTGAGCTG 480
DB 421 GACCAAGATCATTTGGGCTATGAGAGGCAACCGCCCTGGCCCGGGGTGTCCTGAGCTG 480
QY 481 GGGGGCCGCTTCCAGATCCCCGGGTGATATCCGCCCCCACTGCGCGCTTCTGCCCCGCC 540
DB 481 GGGGGCCGCTTCCAGATCCCCGGGTGATATCCGCCCCCACTGCGCGCTTCTGCCCCGCC 540
QY 541 CTGCGCCCCCTGGAATCTCTTGGGCTTCCAGCTCCGCGCGCTCCCAAGATGCGCTGCGC 600
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QY 601 AACCAATGCGCAGATGTGCACTGACCTGCTCTTGGGCTTGAAGATGCTTGGGCTCC 660
DB 601 AACCAATGCGCAGATGTGCACTGACCTGCTCTTGGGCTTGAAGATGCTTGGGCTCC 660
QY 661 GGGCGGGAGTACCGGGCTCTGCACTGCACTGCACTGCGGGGCTGCAAGGTGTCGGGCT 720
DB 661 GGGCGGGAGTACCGGGCTCTGCACTGCACTGCACTGCGGGGCTGCAAGGTGTCGGGCT 720
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DB 721 TCGAGACACTGTGGAAGGCAACGTTTCCCTGCGAGATCCAGTGGTTCACTCACTCAGC 780
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DB 781 ACCGCTTTTGCAGAGTTGACAGAGGCTTTGGGGCGCCCGGAGAGGCTTGCGCTGTTGCC 840

QY 841 GCTTTCTGAGAGAGGCCCCGAGAGAAAAAGTGCCTATGAGCACTGCTGCTCGCTTG 900
DB 841 GCTTTCTGAGAGAGGCCCCGAGAGAAAAAGTGCCTATGAGCACTGCTGCTCGCTTG 900
QY 901 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTGAGGCTCCAGAGACTGAGATATCTGCACTC 960
DB 901 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTGAGGCTCCAGAGACTGAGATATCTGCACTC 960
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QY 1141 GCGAGCAGCCTTTGAATGAGGCGAGTGAATGAGGCTTCCCTGCTGAGTGAACAGC 1200
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QY 1441 GAGCGGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
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US-09-967-237-1
; Sequence 1, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: NM Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)

Query Match 100.0%; Score 1522; DB 18; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 GAAGTTAACTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTTACTTACT 360
301 GAAGTTAACTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTTACTTACT 360
361 GAGGCTCTGAGAGTCTCAGAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAGAT 420
361 GAGGCTCTGAGAGTCTCAGAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAGAT 420
421 GACAGAGTCAATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
421 GACAGAGTCAATGAGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
481 GGGGGGGGCTTCCAGTCCCGGAGTATCCCGGCTCCAGTCCCGGCTCCAGTCCCGG 540
481 GGGGGGGGCTTCCAGTCCCGGAGTATCCCGGCTCCAGTCCCGGCTCCAGTCCCGG 540
541 CTGCGCCCGCTGAGATCTCTGAGGCTTCCAGTCCCGGCTCCAGTCCCGGCTCCAG 600
541 CTGCGCCCGCTGAGATCTCTGAGGCTTCCAGTCCCGGCTCCAGTCCCGGCTCCAG 600
601 AACATGCGCAAGTGTGCACTGACCTGCTCTGAGGCTGAGAGATGCTGAGGCTCC 660
601 AACATGCGCAAGTGTGCACTGACCTGCTCTGAGGCTGAGAGATGCTGAGGCTCC 660
661 GGGGGGGGATCCCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 720
661 GGGGGGGGATCCCGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 720
721 TCGAGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 TCGAGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 ACCGCTTTTGGCAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 ACCGCTTTTGGCAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 GCGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 GCGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
901 GAAAGAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 GAAAGAAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 CTGCGCTGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
961 CTGCGCTGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020

1021 GCCCAGAGTGTATCTGAGATGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 GCCCAGAGTGTATCTGAGATGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 CACACCTCTCTGAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 CACACCTCTCTGAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 GCGACGACCTTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1141 GCGACGACCTTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1201 AGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1201 AGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1261 GCGCTGTTTGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1261 GCGCTGTTTGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1321 AGGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1321 AGGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1381 ACTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1381 ACTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1441 GAGAGCGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 GAGAGCGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 TTTTAAATTAATTAATTAAT 1522
1501 TTTTAAATTAATTAATTAAT 1522

RESULT 4
US-10-888-694-1
Sequence 1, Application US/10888694
Publication No. US2005003425A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 465 California Street, Suite 450
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/888,694
FILING DATE: 08-Jul-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-Jan-2001
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
us-10-888-694-1

Query Match 100.0%; Score 1522; DB 18; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGGCC 60
1 AAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGGCC 60
61 CCGTCCAGGCTCACTGTCAGTCTGTCATCTGCTGTTGATGCTGTCAT 120
61 CCGTCCAGGCTCACTGTCAGTCTGTCATCTGCTGTTGATGCTGTCAT 120
121 CCCGAGAGTTGCCCCGATGTCAGAGATTTCCCTTGGAGAGAGCTTTCTGGAGAA 180
121 CCCGAGAGTTGCCCCGATGTCAGAGATTTCCCTTGGAGAGAGCTTTCTGGAGAA 180
181 GATGACCCACTGGGCGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
181 GATGACCCACTGGGCGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
241 CCACCCGAGAGAGAGATCTACCTGAGAGAGATCTACCTGAGAGAGATCTACCT 300
241 CCACCCGAGAGAGAGATCTACCTGAGAGAGATCTACCTGAGAGAGATCTACCT 300
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301 GAAGTTAAGCTTAATCAGAGAGAGAGCTCCCTGAAGTTAGAGATCTACCTATGTT 360
361 GAGGCTCCGAGATCTCTCAAGAACCCAGATTAATGAGAGAGAGAGAGAT 420
361 GAGGCTCCGAGATCTCTCAAGAACCCAGATTAATGAGAGAGAGAGAGAT 420
421 GACCAAGTCAATTGCGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
421 GACCAAGTCAATTGCGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
481 GCGGCGCGCTTCCAGTCCCGGATGATTCGCCAGTCCCGGCTTTCGCGGCC 540
481 GCGGCGCGCTTCCAGTCCCGGATGATTCGCCAGTCCCGGCTTTCGCGGCC 540
541 CCGCGCCCTGGAATCTCTGAGCTCCAGCTCCCGGCTCCCAAGATCGGCTGCGC 600
541 CCGCGCCCTGGAATCTCTGAGCTCCAGCTCCCGGCTCCCAAGATCGGCTGCGC 600
601 AACCAATGAGCAGTGTGCACTGACCTGCTCTGAGGCTAGAGATGCTCTGAGTCC 660
601 AACCAATGAGCAGTGTGCACTGACCTGCTCTGAGGCTAGAGATGCTCTGAGTCC 660
661 GAGCGGAGAGTCCGAGCTCTGAGCTGATCTGAGGAGGCTGAGAGTCTGCGGCG 720
661 GAGCGGAGAGTCCGAGCTCTGAGCTGATCTGAGGAGGCTGAGAGTCTGCGGCG 720
721 TCGAGACACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 TCGAGACACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 ACCGCTTTGCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 ACCGCTTTGCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

841 GCCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 GCCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
901 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 CCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
961 CCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
1021 GCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 GCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 CACACCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 CACACCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1141 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1201 AGTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1201 AGTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1261 GCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
1261 GCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
1321 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1321 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1381 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1381 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1441 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1441 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1501 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1522
1501 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1522

RESULT 5
US-09-954-456-89
Sequence 89, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 89
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-89

Query Match 100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGAGTGGCTCCCTGTGCCCCAGCCCTGCTCTCTGTGATCCCGGCC 60
DB 31 ACAGTCAGCCGAGTGGCTCCCTGTGCCCCAGCCCTGCTCTCTGTGATCCCGGCC 90
QY 61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCGAGAGGTTCCCGGAGTGAAGAGATTTCCCTTGGAGAGGCTCTTCTGGGGA 180
DB 151 CCCGAGAGGTTCCCGGAGTGAAGAGATTTCCCTTGGAGAGGCTCTTCTGGGGA 210
QY 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT 300
DB 271 CCACCCGAGAGAGAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 390
QY 361 GAGGCTCTGTGAGATCTCTAAGAACCCCAATATATGCCACAGGACAAAGAGAGAT 420
DB 391 GAGGCTCTGTGAGATCTCTAAGAACCCCAATATATGCCACAGGACAAAGAGAGAT 450
QY 421 GACGAGATCATTTGGGCTATGAGAGGCAACCCGCTGGGCTCCGAGGCTGCCAGCTGC 480
DB 451 GACGAGATCATTTGGGCTATGAGAGGCAACCCGCTGGGCTCCGAGGCTGCCAGCTGC 510
QY 481 GCGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCCAAGCTCGCGCTTTCGCCCGGCC 540
DB 511 GCGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCCAAGCTCGCGCTTTCGCCCGGCC 570
QY 541 CTGCGCCCTTGAAGTCTCTGGGCTTCCAGCTCCGCGCTCCCAAGATCTGCGCTGCGC 600
DB 571 CTGCGCCCTTGAAGTCTCTGGGCTTCCAGCTCCGCGCTCCCAAGATCTGCGCTGCGC 630
QY 601 AACCAATGGCAGATGTGCACTGACCCGCTCTGGGCTGAGATGGCTCTGGGCTGCC 660
DB 631 AACCAATGGCAGATGTGCACTGACCCGCTCTGGGCTGAGATGGCTCTGGGCTGCC 690
QY 661 GGGCGGAGATACCGGGCTCTGAGCTGATCTGCACTGGGCGGCTGCAAGTGTCCGGGC 720
DB 691 GGGCGGAGATACCGGGCTCTGAGCTGATCTGCACTGGGCGGCTGCAAGTGTCCGGGC 750
QY 721 TCGGAGCACTGTGGAAGGCCACCGTTTCCCTGCCAGATTCAGAGTGTCACTCAGC 780
DB 751 TCGGAGCACTGTGGAAGGCCACCGTTTCCCTGCCAGATTCAGAGTGTCACTCAGC 810
QY 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCGCTGCTGTTGGCC 840

DB 811 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGCGCCCGGAGAGCTGCGCTGTTGGCC 870
QY 841 GCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTATGACAGTTGCTGTGCTTG 900
DB 871 GCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTATGACAGTTGCTGTGCTTG 930
QY 901 GAGAAATCGCTGAGAGAGGCTCAGAGATCAGGTGCCAGAGATGAGATATCTGCACTC 960
DB 931 GAGAAATCGCTGAGAGAGGCTCAGAGATCAGGTGCCAGAGATGAGATATCTGCACTC 990
QY 961 CTGCTCTGACCTTCAGCGGCTACTTCCATATATGAGGAGTCTGACTACACCGGCTGT 1020
DB 991 CTGCTCTGACCTTCAGCGGCTACTTCCATATATGAGGAGTCTGACTACACCGGCTGT 1050
QY 1021 GCCCAGGAGTATCTGAGTGTGTGTTTAAACAGACAGTATGATGTAGTCTTAAGCAGCTC 1080
DB 1051 GCCCAGGAGTATCTGAGTGTGTGTTTAAACAGACAGTATGATGTAGTCTTAAGCAGCTC 1110
QY 1081 CACACCTCTCTGACACCTCTGTGGGACCTGTGATCTCGGCTACAGCTGAATCTTCGA 1140
DB 1111 CACACCTCTCTGACACCTCTGTGGGACCTGTGATCTCGGCTACAGCTGAATCTTCGA 1170
QY 1141 GCGAGCAGCCTTTGAATGGGCGAGTATGAGGCTCTCCCTGCTGAGTGAAGCAGC 1200
DB 1171 GCGAGCAGCCTTTGAATGGGCGAGTATGAGGCTCTCCCTGCTGAGTGAAGCAGC 1230
QY 1201 AGTCTCGGAGTGTGACACAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTA 1260
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QY 1261 GCCCTGTTTTGGCTCTCTTTTGTCTGTCAACAGCGTGGGCTTCTTGTGCAATGGA 1320
DB 1291 GCCCTGTTTTGGCTCTCTTTTGTCTGTCAACAGCGTGGGCTTCTTGTGCAATGGA 1350
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DB 1351 AGGCGACAGAGAGGAGCAACAAAGGGGTGTGAGCTACCGCCAGCAGAGTACCGCAG 1410
QY 1381 ACTGAGCTTGAAGGCTGATCTTGAAGATGTGAAGAACAGCAGCAGAGGATCTGAGGG 1440
DB 1411 ACTGAGCTTGAAGGCTGATCTTGAAGATGTGAAGAACAGCAGCAGAGGATCTGAGGG 1470
QY 1441 GAGCGGCTTAATCTGTCTGTCTCTCTATATGCACTTCTTTTAATGCAAGAAAT 1500
DB 1471 GAGCGGCTTAATCTGTCTGTCTCTCTATATGCACTTCTTTTAATGCAAGAAAT 1530
QY 1501 TTTTAAATTAATATTTATAT 1522
DB 1531 TTTTAAATTAATATTTATAT 1552

RESULT 6
US-09-954-456-726
Sequence 726, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cane
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 726
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-726

Query Match 100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGCTCCCTGTCGCGCCAGCCCTGCTCCCTGTTGATCCCGCC 60
DB 31 ACAGTCAGCCGATGCTCCCTGTCGCGCCAGCCCTGCTCCCTGTTGATCCCGCC 90
QY 61 CCTGCTCCAGGCTCTGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCTGCTCCAGGCTCTGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCCAAGGTTGCCCCGATGCAAGAGATTCCCCCTGGAGAGAGGCTCTTCTGGAGAA 180
DB 151 CCCCAAGGTTGCCCCGATGCAAGAGATTCCCCCTGGAGAGAGGCTCTTCTGGAGAA 210
QY 181 GATGATCCACTGCGGCAAGAGATCTGCCAGTGAAGAGATTCACTCCAGAGAGAGAT 240
DB 211 GATGATCCACTGCGGCAAGAGATCTGCCAGTGAAGAGATTCACTCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 271 CCACCCGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACCTAGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACCTAGTT 390
QY 361 GAAGCTCTGAGAGATCTTCAAGAACTCCAGAAATATGCCCAAGGAGCAAAAGAGGAG 420
DB 391 GAAGCTCTGAGAGATCTTCAAGAACTCCAGAAATATGCCCAAGGAGCAAAAGAGGAG 450
QY 421 GACCAAGATCTTTGGGCTATGAGAGGCAACCGGCTGCGCCCGGCTGCTCCAGGCTGC 480
DB 451 GACCAAGATCTTTGGGCTATGAGAGGCAACCGGCTGCGCCCGGCTGCTCCAGGCTGC 510
QY 481 GGGGGCGCTTCCAGTCCCGGCTGATTCGGCCCGCCAGCTGCGGCTTCTGCGCGGCG 540
DB 511 GGGGGCGCTTCCAGTCCCGGCTGATTCGGCCCGCCAGCTGCGGCTTCTGCGCGGCG 570
QY 541 CTGCGGCGCTTCCAGTCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC 600
DB 571 CTGCGGCGCTTCCAGTCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC 630
QY 601 AACCAATGCGCAAGTGTGCACTGACCTGCTCTGCGGCTGAGATGCTCTGCGGTCC 660
DB 631 AACCAATGCGCAAGTGTGCACTGACCTGCTCTGCGGCTGAGATGCTCTGCGGTCC 690
QY 661 GGGCGGAGATCCGGGCTCTGAGCTGCACTGCACTGCGGAGGCTCAGAGTCTCCGGG 720
DB 691 GGGCGGAGATCCGGGCTCTGAGCTGCACTGCACTGCGGAGGCTCAGAGTCTCCGGG 750
QY 721 TCGAGACACATGTGAGAGCCACCGTTTCCCTGCGAGATCCACGTGTTCACTCAAC 780
DB 751 TCGAGACACATGTGAGAGCCACCGTTTCCCTGCGAGATCCACGTGTTCACTCAAC 810

QY 781 ACCGCTTGGCAGATTGACAGAGGCTTGGGGGCGCCCGGAGAGCCCTGCGGTTGGCC 840
DB 811 ACCGCTTGGCAGATTGACAGAGGCTTGGGGGCGCCCGGAGAGCCCTGCGGTTGGCC 870
QY 841 GCCTTCTGAGAGAGGCGCCGAGAGAAACAGTCCCTATGAGAGATGCTGCTGCTG 900
DB 871 GCCTTCTGAGAGAGGCGCCGAGAGAAACAGTCCCTATGAGAGATGCTGCTGCTG 930
QY 901 GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGTCCAGAGATGCAATATTCGACTC 960
DB 931 GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGTCCAGAGATGCAATATTCGACTC 990
QY 961 CTGCGCTCTGACTGACCGGCTACTTCAATATGAGAGGCTCTGCTCAACCGGCTG 1020
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DB 1051 GCCCAGGATGCTGATCTGATGCTGTTTAAACAGACAGATGCTGATGCTGAGAGCTC 1110
QY 1081 CACACCTCTCTGACACCTCTGAGGAGCTGCTGATCTGCTGCTGCTGCTGCTGCTG 1140
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DB 1411 ACTGAGCTTGAAGGCTGATCTTGAAGATGAGAGCCAGCCAGAGGATCTGAGG 1470
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DB 1471 GAGGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1530
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DB 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 7
US-09-960-706-1080
Sequence 1080, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
APPLICANT: Manger, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1080
LENGTH: 1552

Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCCGATGATGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGGC 60
Db ACAGTCAGCCGATGATGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGGC 90

61 CTTGCTCCAGGCTTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db CTTGCTCCAGGCTTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150

121 CCCCAGAGGTTGCCCCGATGAGAGAGATTTCCCTTTGGAGAGAGGCTCTTCTGGGGA 180
Db CCCCAGAGGTTGCCCCGATGAGAGAGATTTCCCTTTGGAGAGAGGCTCTTCTGGGGA 210

181 GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
Db GATGACCCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 270

241 CCAGCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
Db CCAGCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330

301 GAAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 360
Db GAAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 390

361 GAGGCTCTGAGAGATCTCTCAAGAACCCAGAAATTAATGCCACAGGAGCAAAAGAGGAT 420
Db GAGGCTCTGAGAGATCTCTCAAGAACCCAGAAATTAATGCCACAGGAGCAAAAGAGGAT 450

421 GACCAAGATCAATGGGCTATGAGAGGCGACCCGCGCTGAGCCCTGGGTGCTCCCAAGCTGC 480
Db GACCAAGATCAATGGGCTATGAGAGGCGACCCGCGCTGAGCCCTGGGTGCTCCCAAGCTGC 510

481 GGGGGGCGCTTCAAGTCCCCGGTGAATACCGCCCCCACTGGCGCTTGGCCCGGC 540
Db GGGGGGCGCTTCAAGTCCCCGGTGAATACCGCCCCCACTGGCGCTTGGCCCGGC 570

541 CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGC 600
Db CTGGCGCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGC 630

601 AACAAATGGCCAGATGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db AACAAATGGCCAGATGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690

661 GGGCGGAGATACCGGCTCTGCAAGCTGCACTGCACTGGGGGCTGCAAGTGTCTCGGCG 720
Db GGGCGGAGATACCGGCTCTGCAAGCTGCACTGCACTGGGGGCTGCAAGTGTCTCGGCG 750

721 TGGAGCACTGTGAGAGGCCACCGTTCCCTGCGAGATCCAGTGGTTCACCTCAGC 780
Db TGGAGCACTGTGAGAGGCCACCGTTCCCTGCGAGATCCAGTGGTTCACCTCAGC 810

781 ACCGCTTTGCAAGATTGACGAGGCTTGGGGCGCCCGGAGAGGCTGCGCGTGGGC 840
Db ACCGCTTTGCAAGATTGACGAGGCTTGGGGCGCCCGGAGAGGCTGCGCGTGGGC 870

841 GCGCTTCTGAGAGAGGCGCCGAGAGAAACAGTGGCTTATGAGAGTGTGCTGCTGCTG 900
Db GCGCTTCTGAGAGAGGCGCCGAGAGAAACAGTGGCTTATGAGAGTGTGCTGCTGCTG 930

901 GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGTCCAGGACTGAGCAATATCTGACATC 960
Db GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGTCCAGGACTGAGCAATATCTGACATC 990

961 CTGCGCTCTGACTTCAAGCGCTAATTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db CTGCGCTCTGACTTCAAGCGCTAATTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050

1021 GCCCAGGAGTCACTGAGCTGTGTTTAAACAGACAGATGATGATGCTAAGCAGCTC 1080
1051 GCCCAGGAGTCACTGAGCTGTGTTTAAACAGACAGATGATGATGCTAAGCAGCTC 1110

1081 CACACCTTCTGACACCCCTGTGGGAGCTGTGAGCTTGGCTTCAAGCTGAATCTTCCGA 1140
Db CACACCTTCTGACACCCCTGTGGGAGCTGTGAGCTTGGCTTCAAGCTGAATCTTCCGA 1170

1141 GCGAGCAGGCTTTGAATGGGAGATGATGAGGCTCTTCCCTGCTGAGATGAGCAGC 1200
Db GCGAGCAGGCTTTGAATGGGAGATGATGAGGCTCTTCCCTGCTGAGATGAGCAGC 1230

1201 AGTCTCGGAGCTGAGAGCAATGAGCTGAATTCCTGCTGAGCTGAGTGAATCTCTA 1260
Db AGTCTCGGAGCTGAGAGCAATGAGCTGAATTCCTGCTGAGCTGAGTGAATCTCTA 1290

1261 GCCCTGTTTTGAGCTCTTTTTCCTGTCACAGAGCTGAGCTTCTTGTGAGATGAGA 1320
Db GCCCTGTTTTGAGCTCTTTTTCCTGTCACAGAGCTGAGCTTCTTGTGAGATGAGA 1350

1321 AGGCAAGCAGAGAGGAGAACAAAGGGGTGTGAGCTACCGCCAGAGAGTACCCGAG 1380
Db AGGCAAGCAGAGAGGAGAACAAAGGGGTGTGAGCTACCGCCAGAGAGTACCCGAG 1410

1381 ACTGAGCCTAGAGGCTGATCTTGAAGATGAGAGCCAGCCAGAGGATCTGAGG 1440
Db ACTGAGCCTAGAGGCTGATCTTGAAGATGAGAGCCAGCCAGAGGATCTGAGG 1470

1441 GAGGCGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db GAGGCGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530

1501 TTTTAAATTAATTTATTAAT 1522
Db TTTTAAATTAATTTATTAAT 1552

RESULT 9

US-09-968-007A-213
; Sequence 213, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebnert, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 213
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-213

Query Match 100.0%; Score 1522; DB 11; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCCGATGATGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGGC 60

Db 31 AAGTATGAGCGATGAGCTCCCTGTCCTCCAGCCCTGAGCTCTCTGTGTATCCCGACC 90
Qy 61 CCTGTCCAGGCTCACTGTGCAACTGTGCTGTCACTGCTGTTCTGTATGCTGTCAAT 120
Db 91 CCGTGTCCAGGCTCACTGTGCAACTGTGCTGTCACTGCTGTTCTGTATGCTGTCAAT 150
Qy 121 CCCCAGAGGTTGCCCCGAGTGCAGAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGAA 180
Db 151 CCCCAGAGGTTGCCCCGAGTGCAGAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGAA 210
Qy 181 GATGACCCACTGGGCGAGAGAGATTCGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 240
Db 211 GATGACCCACTGGGCGAGAGAGATTCGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 270
Qy 241 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
Db 271 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
Qy 301 GAAATTAACTTAATCAGAAAGAGGCTCCCTGAATTAAGAGATCTACCTACTGTT 360
Db 331 GAAATTAACTTAATCAGAAAGAGGCTCCCTGAATTAAGAGATCTACCTACTGTT 390
Qy 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAATGCCAGAGGAGCAAGAGAGGAGAT 420
Db 391 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAATGCCAGAGGAGCAAGAGAGGAGAT 450
Qy 421 GACCAAGATCAATTGGGCTATGAGAGGCAACCCGCTGAGCCCGGGTGTCCCAAGCTGC 480
Db 451 GACCAAGATCAATTGGGCTATGAGAGGCAACCCGCTGAGCCCGGGTGTCCCAAGCTGC 510
Qy 481 GGGGGCGGCTTCAAGTCCCCGGTGAATACCCGCCCACTGCGGCTTCTGCCCCGGC 540
Db 511 GGGGGCGGCTTCAAGTCCCCGGTGAATACCCGCCCACTGCGGCTTCTGCCCCGGC 570
Qy 541 CTGCGCCCCCTGAAACTCTGTGGGCTTCAAGTCCGCGCCCTCCAGAACTGGGCTGCGC 600
Db 571 CTGCGCCCCCTGAAACTCTGTGGGCTTCAAGTCCGCGCCCTCCAGAACTGGGCTGCGC 630
Qy 601 AACAAATGCGCAAGTGTGCAACTGACCCCTGCTCTGGGCTTGAAGATGGCTGTGGGTCGC 660
Db 631 AACAAATGCGCAAGTGTGCAACTGACCCCTGCTCTGGGCTTGAAGATGGCTGTGGGTCGC 690
Qy 661 GGGGGCGGAGTACCGGGCTGTGAGCTGCACTGAGCTGGGGGGCTGCGAGTGTCCGGGC 720
Db 691 GGGGGCGGAGTACCGGGCTGTGAGCTGCACTGAGCTGGGGGGCTGCGAGTGTCCGGGC 750
Qy 721 TCGGAGCACTGTGGAAGGCCACGTTTCCCTGCGAGATCAAGTGTGTTCACTCAAC 780
Db 751 TCGGAGCACTGTGGAAGGCCACGTTTCCCTGCGAGATCAAGTGTGTTCACTCAAC 810
Qy 781 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGCGCCCGGAGAGGCTGCTGTTGGCC 840
Db 811 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGCGCCCGGAGAGGCTGCTGTTGGCC 870
Qy 841 GCGTTTCTGAGAGAGGGCCCGAAGAAACAGTGCCTATGACAGTGTGCTGTGCTGG 900
Db 871 GCGTTTCTGAGAGAGGGCCCGAAGAAACAGTGCCTATGACAGTGTGCTGTGCTGG 930
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAAGAGCTCAGGTCCAGAGCTGAGACATATCTGACATC 960
Db 931 GAAAGAAATGCTGAGAGAGGCTCAAGAGCTCAGGTCCAGAGCTGAGACATATCTGACATC 990
Qy 961 CTGCGCTCTGACTTCAAGCGGCTACTTCCAAATTAAGGGGTCTGTGACTACACCGCCCTGT 1020
Db 991 CTGCGCTCTGACTTCAAGCGGCTACTTCCAAATTAAGGGGTCTGTGACTACACCGCCCTGT 1050
Qy 1021 GCCCAAGGGTGCATCTGAGCTGTGTTTACAGAGAGTGAATGCTAGAGTGAAGAGCTC 1080
Db 1051 GCCCAAGGGTGCATCTGAGCTGTGTTTACAGAGAGTGAATGCTAGAGTGAAGAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGTGACTCTGCGCTACAGCTGAATCTTCGA 1140

Db 1111 CACACCTCTCTGACACCTCTGTGGGAGCTGTGTGACTCTGCGCTACAGTGAATCTTCGA 1170
Qy 1141 GCGAGCAGCCTTTGAATGGGCGAGTGAATTAAGGCTCTTCCCTGCTGAGTGAACAGC 1200
Db 1171 GCGAGCAGCCTTTGAATGGGCGAGTGAATTAAGGCTCTTCCCTGCTGAGTGAACAGC 1230
Qy 1201 AGTCTCGGCGTGTGACAGCAGTCCAGTGAATTTCTTCCCTGCTGCTGTGACATCTCTA 1260
Db 1231 AGTCTCGGCGTGTGACAGCAGTCCAGTGAATTTCTTCCCTGCTGCTGTGACATCTCTA 1290
Qy 1261 GCCCTGTTTTTGGGCTCTTTTGTGCTGTCAACAGCGTCGGGTTCTTGTGCAATGAGA 1320
Db 1291 GCCCTGTTTTTGGGCTCTTTTGTGCTGTCAACAGCGTCGGGTTCTTGTGCAATGAGA 1350
Qy 1321 AGGAGCAGAGAGGAGAACCAAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGAGCAGAGAGGAGAACCAAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1410
Qy 1381 ACTGAGGCTGAGAGGCTGTGAGTCTTGAAGAAATGTGAAGAACCAAGGAGATCTGAGG 1440
Db 1411 ACTGAGGCTGAGAGGCTGTGAGTCTTGAAGAAATGTGAAGAACCAAGGAGATCTGAGG 1470
Qy 1441 GAGCGGCTAACTGTCTGTCTGCTCAATTAAGCACTTCTTTAACTGCAAGAAAT 1500
Db 1471 GAGCGGCTAACTGTCTGTCTGCTCAATTAAGCACTTCTTTAACTGCAAGAAAT 1530
Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 10
US-10-301-822-11
; Sequence 11, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RMM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43) ... (1422)
US-10-301-822-11

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTATGAGCGATGAGCTCCCTGTCCTCCAGCCCTGAGCTCTCTGTGTATCCCGACC 60

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Db 31 ACAGTCACGCGGATGAGTCCCTGTCGCCCCAGCCCCCTGCGCTCCCTGTTGATCCCGGCC 90
Qy 61 CCTGCTCCAGGCGCTGACCTGTGTGAACCTGCTGTGACCTGCTGCTTCTGTATGCTGTGCAT 120
Db 91 CTTGCTCCAGGCGCTGACCTGTGTGAACCTGCTGTGACCTGCTGCTTCTGTATGCTGTGCAT 150
Qy 121 CCCGAGAGGTTTCCCGGATGACAGAGATTTCCCTTTGGAGAGAGCTCTTCTGCGGGA 180
Db 151 CCCGAGAGGTTTCCCGGATGACAGAGATTTCCCTTTGGAGAGAGCTCTTCTGCGGGA 210
Qy 181 GATGACCCACTGAGGCGAGAGAGATCTGCGCACTGAAGAGATTTCAACCCAGAGAGAGAT 240
Db 211 GATGACCCACTGAGGCGAGAGAGATCTGCGCACTGAAGAGATTTCAACCCAGAGAGAGAT 270
Qy 241 CCAACCCGAGAGAGAGATTTCTACTGTAGAGAGATTTCTACTGTAGAGAGAGATTTCACT 300
Db 271 CCAACCCGAGAGAGAGATTTCTACTGTAGAGAGATTTCTACTGTAGAGAGAGATTTCACT 330
Qy 301 GAAATTAAAGCTTAATCAGAGAGAGAGCTCCCTGAAGTTAGAGATTTCACTACTGTT 360
Db 331 GAAATTAAAGCTTAATCAGAGAGAGAGCTCCCTGAAGTTAGAGATTTCACTACTGTT 390
Qy 361 GAGGCTCTGAGAGATCTCTCAAGAACCCAGAAATATGCCCACAGGACAAAGAGAGAT 420
Db 391 GAGGCTCTGAGAGATCTCTCAAGAACCCAGAAATATGCCCACAGGACAAAGAGAGAT 450
Qy 421 GACGAGAGTCAATTTGGGCTATGAGAGGCGACCCGCTGCGGCTGCGGCTGCGGCTGCG 480
Db 451 GACGAGAGTCAATTTGGGCTATGAGAGGCGACCCGCTGCGGCTGCGGCTGCGGCTGCG 510
Qy 481 GGGGGCGGCTTCAAGTCCCGGCTGATTCGCGCCCCAGCTGCGGCTTCTGCGCGGCC 540
Db 511 GGGGGCGGCTTCAAGTCCCGGCTGATTCGCGCCCCAGCTGCGGCTTCTGCGCGGCC 570
Qy 541 CTGCGCCCCCTGGAATCTCTGCGGCTTCTCAAGTCCCGGCTGCGGCTGCGGCTGCGG 600
Db 571 CTGCGCCCCCTGGAATCTCTGCGGCTTCTCAAGTCCCGGCTGCGGCTGCGGCTGCGG 630
Qy 601 AACAAATGCGCAAGTGTGCACTGACCTGCTGCTGCGGCTGAGATGCTGCGGCTGCGG 660
Db 631 AACAAATGCGCAAGTGTGCACTGACCTGCTGCTGCGGCTGAGATGCTGCGGCTGCGG 690
Qy 661 GGGCGGAGATCCGGGCTGAGAGCTGACCTGACCTGACCTGAGGAGGCTGAGGAGG 720
Db 691 GGGCGGAGATCCGGGCTGAGAGCTGACCTGACCTGACCTGAGGAGGCTGAGGAGG 750
Qy 721 TCGGAGCACTGTGTGAAGGCAACCTTTCCTGCGGAGATCCACTGTGTTCACTCAAC 780
Db 751 TCGGAGCACTGTGTGAAGGCAACCTTTCCTGCGGAGATCCACTGTGTTCACTCAAC 810
Qy 781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGTGGGCGCCCGGAGAGGCTGCGGCTTGTGG 840
Db 811 ACCGCTTTTGCAGAGTTGACAGAGGCTTGTGGGCGCCCGGAGAGGCTGCGGCTTGTGG 870
Qy 841 GCTTTTGTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGAGAGATGCTGTGCTGCTG 900
Db 871 GCTTTTGTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGAGAGATGCTGTGCTGCTG 930
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGACTGAGCAATCTGCACTC 960
Db 931 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGAGTCCAGAGACTGAGCAATCTGCACTC 990
Qy 961 CTGCGCTGCTGACTTCAAGCGGCTTCTTCAATATGAGGAGTCTCTGACATCAACCGCTGT 1020
Db 991 CTGCGCTGCTGACTTCAAGCGGCTTCTTCAATATGAGGAGTCTCTGACATCAACCGCTGT 1050
Qy 1021 GCGCAGGAGTGTATCTGAGCTGTGTTTAAACAGACAGTATGCTGAGTGTCTAAGCAGCTC 1080
Db 1051 GCGCAGGAGTGTATCTGAGCTGTGTTTAAACAGACAGTATGCTGAGTGTCTAAGCAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTCTGTGTGGAGCTGTGTGACTCTCTGCTGACGTGAACCTTCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGTGTGGAGCTGTGTGACTCTCTGCTGACGTGAACCTTCCGA 1170

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Qy 1141 GCGAGCAGCCTTTGAATGAGGAGATTTGAGGCTCTTCTCTGCTGAGTGAACAGC 1200
Db 1171 GCGAGCAGCCTTTGAATGAGGAGATTTGAGGCTCTTCTCTGCTGAGTGAACAGC 1230
Qy 1201 AGTCTCGGAGCTGCTGAGGCACTGCACTGAATTCCTGCTGCTGCTGCTGCTGATCTTA 1260
Db 1231 AGTCTCGGAGCTGCTGAGGCACTGCACTGAATTCCTGCTGCTGCTGCTGCTGATCTTA 1290
Qy 1261 GCGCTGCTTTTGGCTCTCTTTTGTGCTGACACAGCTGCGCTTCTTGTGAGATGAA 1320
Db 1291 GCGCTGCTTTTGGCTCTCTTTTGTGCTGACACAGCTGCGCTTCTTGTGAGATGAA 1350
Qy 1321 AGGACACAGAGGAGGAAACAAAGGAGTGTGAGCTACCGCCAGCAGAGGTAAGCCGAG 1380
Db 1351 AGGACACAGAGGAGGAAACAAAGGAGTGTGAGCTACCGCCAGCAGAGGTAAGCCGAG 1410
Qy 1381 ACTGAGCCTTAGAGGCTGAGTCTTGAAGATGTGAAGAACCCAGACAGAGCATTTGAGG 1440
Db 1411 ACTGAGCCTTAGAGGCTGAGTCTTGAAGATGTGAAGAACCCAGACAGAGCATTTGAGG 1470
Qy 1441 GAGCGCGTAACTGTCTGTCTCTGCTCATTAATGCACTTCTTTTAATGCAAGAAAT 1500
Db 1471 GAGCGCGTAACTGTCTGTCTCTGCTCATTAATGCACTTCTTTTAATGCAAGAAAT 1530
Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAAT 1552

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RESULT 11
US-10-465-572-9
; Sequence 9, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250, 00012
; CURRENT APPLICATION NUMBER: US/10/465, 572
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201, 642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307, 600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-465-572-9

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Query Match 100.0%; Score 1522; DB 15; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0; Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ACAGTCACGCGGATGAGTCCCTGTCGCCCCAGCCCCCTGCGCTCCCTGTTGATCCCGGCC 60
Db 31 ACAGTCACGCGGATGAGTCCCTGTCGCCCCAGCCCCCTGCGCTCCCTGTTGATCCCGGCC 90
Qy 61 CCTGCTCCAGGCGCTGACCTGTGTGAACCTGCTGTGACCTGCTGCTTCTGTATGCTGTGCAT 120
Db 91 CTTGCTCCAGGCGCTGACCTGTGTGAACCTGCTGTGACCTGCTGCTTCTGTATGCTGTGCAT 150
Qy 121 CCCGAGAGGTTTCCCGGATGACAGAGATTTCCCTTTGGAGAGAGCTCTTCTGCGGGA 180
Db 151 CCCGAGAGGTTTCCCGGATGACAGAGATTTCCCTTTGGAGAGAGCTCTTCTGCGGGA 210
Qy 181 GATGACCCACTGAGGCGAGAGAGATCTGCGCACTGAAGAGATTTCAACCCAGAGAGAGAT 240
Db 211 GATGACCCACTGAGGCGAGAGAGATCTGCGCACTGAAGAGATTTCAACCCAGAGAGAGAT 270

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QY 241 CCAACCGAGAGAGATCTACCTGAGAGAGATCTACCTGAGAGAGATCTACCT 300
DB 271 CCAACCGAGAGAGATCTACCTGAGAGAGATCTACCTGAGAGAGATCTACCT 330
QY 301 GAAATTAAAGCTTAATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 331 GAAATTAAAGCTTAATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
QY 361 GAGGCTCTGAGAGATCTCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 391 GAGGCTCTGAGAGATCTCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
QY 421 GAGCAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 451 GAGCAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
QY 481 GCGGAGCGCTTCCAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 511 GCGGAGCGCTTCCAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
QY 541 CTGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 571 CTGCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
QY 601 AACCAATGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 631 AACCAATGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
QY 661 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 691 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
QY 721 TGGGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 751 TGGGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
QY 781 ACCGCGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 811 ACCGCGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
QY 841 GCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 871 GCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 901 GAAAGAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 931 GAAAGAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
QY 961 CTGCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 991 CTGCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
QY 1021 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1051 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
QY 1081 CACACCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1111 CACACCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
QY 1141 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1171 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
QY 1201 AGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1231 AGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
QY 1261 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1291 GCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
QY 1321 AGGCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

DB 1351 AGGCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
QY 1381 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1411 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
QY 1441 GAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1471 GAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530
QY 1501 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1552

RESULT 12
US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US2003022437A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9101-175-999
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SBO ID NOS: 2699
; SBO ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 31 ACAGTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 90
QY 61 CTGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 91 CTGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
QY 121 CCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 151 CCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210
QY 181 GATGACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 211 GATGACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270
QY 241 CCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 271 CCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
QY 301 GAAATTAAAGCTTAATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 331 GAAATTAAAGCTTAATCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390

QY 361 GAGGCTCTGAGATCTCTCAAGAACCCAGAAATATATGCCACAGGAGCAAGAGGGAT 420
DB 391 GAGGCTCTGAGATCTCTCAAGAACCCAGAAATATATGCCACAGGAGCAAGAGGGAT 450
QY 421 GACCAAGATCATTTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGTCCCAAGCTGC 480
DB 451 GACCAAGATCATTTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGTCCCAAGCTGC 510
QY 481 GGGGGCCGCTTCAAGTCCCGGGTGAATACCGCCCGCCAGCTGGCCCTTGGCCCGGC 540
DB 511 GGGGGCCGCTTCAAGTCCCGGGTGAATACCGCCCGCCAGCTGGCCCTTGGCCCGGC 570
QY 541 CTGGCCCCCTGGAATCTCTGGGCTTCAAGTCCCGCCCTCCAGAACTGGCCCTGGCC 600
DB 571 CTGGCCCCCTGGAATCTCTGGGCTTCAAGTCCCGCCCTCCAGAACTGGCCCTGGCC 630
QY 601 AACAAATGACCAAGTGTGCACTGACCTGCTCTGGGCTAGAGATGAGCTTGGGCTCC 660
DB 631 AACAAATGACCAAGTGTGCACTGACCTGCTCTGGGCTAGAGATGAGCTTGGGCTCC 690
QY 661 GGGGGGAGTACCGGCTCTGACAGCTGATCTGCACTGGGGGGCTGACAGTGTCCGGGC 720
DB 691 GGGGGGAGTACCGGCTCTGACAGCTGATCTGCACTGGGGGGCTGACAGTGTCCGGGC 750
QY 721 TCGGAGCACTGTGGAAGGCGCACGCTTCCCTGCGAGATCACTGGTTCACTCAGC 780
DB 751 TCGGAGCACTGTGGAAGGCGCACGCTTCCCTGCGAGATCACTGGTTCACTCAGC 810
QY 781 ACCGCTTTGCGAAGTTGACAGAGGCTTGGGGCGCCGAGAGGCTGCGTGTGGCC 840
DB 811 ACCGCTTTGCGAAGTTGACAGAGGCTTGGGGCGCCGAGAGGCTGCGTGTGGCC 870
QY 841 GCTTTTCTGGAAGAGGGCCCGAGAAACAGTGTCTATGAGCACTGCTGTCTGGCTTG 900
DB 871 GCTTTTCTGGAAGAGGGCCCGAGAAACAGTGTCTATGAGCACTGCTGTCTGGCTTG 930
QY 901 GAAGAATGCTGAGGAAGGCTCAGAGCTCAGGTCCAGAGCTGGAACATCTGCACTC 960
DB 931 GAAGAATGCTGAGGAAGGCTCAGAGCTCAGGTCCAGAGCTGGAACATCTGCACTC 990
QY 961 CTGGCTCTGACTTCAAGCGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
DB 991 CTGGCTCTGACTTCAAGCGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
QY 1021 GCGCAGGGGTGATCTGAGCTGTGTTAACAGACAGTATGTGAGTCTTAAGACAGCTC 1080
DB 1051 GCGCAGGGGTGATCTGAGCTGTGTTAACAGACAGTATGTGAGTCTTAAGACAGCTC 1110
QY 1081 CACACCTCTCTGACACCTGTGGGGGACTGAGTCTCTGGCTACAGTGAATTCGGA 1140
DB 1111 CACACCTCTCTGACACCTGTGGGGGACTGAGTCTCTGGCTACAGTGAATTCGGA 1170
QY 1141 GCGAGCAGCTTTGATGAGGCGAGTGAATGAGCCTCTCTCTGCTGAGTGAACAGC 1200
DB 1171 GCGAGCAGCTTTGATGAGGCGAGTGAATGAGCCTCTCTCTGCTGAGTGAACAGC 1230
QY 1201 AGTCTCTGGGCTGCTGAGCAGTCCAGCTGAATCTCTGCTGGCTGCTGCTGATCTTA 1260
DB 1231 AGTCTCTGGGCTGCTGAGCAGTCCAGCTGAATCTCTGCTGGCTGCTGCTGATCTTA 1290
QY 1261 GCGCTGCTTTGGGCTCTTTTGTGCTGACAGAGTGGCGCTCTCTGCTGAGATGAGA 1320
DB 1291 GCGCTGCTTTGGGCTCTTTTGTGCTGACAGAGTGGCGCTCTCTGCTGAGATGAGA 1350
QY 1321 AGGCAACAGAGAGGGAACAAAGGGGTGTGAGCTACCGCCAGAGAGTGAAGCGAG 1380
DB 1351 AGGCAACAGAGAGGGAACAAAGGGGTGTGAGCTACCGCCAGAGAGTGAAGCGAG 1410
QY 1381 ACTGAGCTTAAGAGGCTGATCTTGGAGAAATGTGAGAACCGCCAGAGGCACTTGAAGG 1440
DB 1411 ACTGAGCTTAAGAGGCTGATCTTGGAGAAATGTGAGAACCGCCAGAGGCACTTGAAGG 1470
QY 1441 GAGGCGGCTTCACTGCTCTGCTCAGTATGAGCACTTCTTTTAACAGCAAGAAAT 1500

DB 1471 GAGGCGGCTTCACTGCTCTGCTCAGTATGAGCACTTCTTTAAGCCAGAAAT 1530
QY 1501 TTTTAAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 13
US-10-388-360-291
; Sequence 291, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffrey B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 291
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-291

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTACGCGGATGAGTCTCTCTGTCGCCAGCCCTGCTGCTCTGTTATCCCGGCC 60
DB 31 ACAGTACGCGGATGAGTCTCTCTGTCGCCAGCCCTGCTGCTCTGTTATCCCGGCC 90
QY 61 CCTGCTCAGGCTCACTGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCTGCTCAGGCTCACTGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCAGAGGTTGCCCGGATGACAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGGA 180
DB 151 CCCAGAGGTTGCCCGGATGACAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGGA 210
QY 181 GATGACCACTGGGCGAGAGGATTTGCCAGTGAAGAGATTTCAACAGAGAGAGAT 240
DB 211 GATGACCACTGGGCGAGAGGATTTGCCAGTGAAGAGATTTCAACAGAGAGAGAT 270
QY 241 CCAACCGAGAGAGAGATTTCACTGAGAGAGATTTCACTGAGAGAGAGATTTCACT 300
DB 271 CCAACCGAGAGAGAGATTTCACTGAGAGAGATTTCACTGAGAGAGAGATTTCACT 330
QY 301 GAAGTTAAGCTTAATCAGAAAGAGGCTCCCTGAAGTTAGAGATTTCACTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAAAGAGGCTCCCTGAAGTTAGAGATTTCACTACTGTT 390
QY 361 GAGGCTCTGAGATCTCTAAGAACCCAGAAATATATGCCACAGGAGCAAGAGGAT 420
DB 391 GAGGCTCTGAGATCTCTAAGAACCCAGAAATATATGCCACAGGAGCAAGAGGAT 450
QY 421 GACCAAGTCAATTTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGTCCCAAGCTGC 480
DB 451 GACCAAGTCAATTTGGGCTATGAGAGCGACCCGCTGGCCCGGGGTGTCCCAAGCTGC 510
QY 481 GGGGGCCGCTTCAAGTCCCGGGTGAATACCGCCCGCCAGCTGGCCCTTGGCCCGGC 540

Db 511 GGGGGCGCTTCCAGTCCCGGAGATCCGCCCCCAGCTGCGCCCTTCTGCCCCGCC 570
Qy 541 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCCTCCAGAACTGCGCCCTGCGC 600
Db 571 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCCTCCAGAACTGCGCCCTGCGC 630
Qy 601 AACAAATGGCAAGTGTGAACTGAAACCCCTGCTCCCTGGGCTAGAAATGCTCTGGGTCCC 660
Db 631 AACAAATGGCAAGTGTGAACTGAAACCCCTGCTCCCTGGGCTAGAAATGCTCTGGGTCCC 690
Qy 661 GGGCGGGAATACCGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 720
Db 691 GGGCGGGAATACCGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 750
Qy 721 TCGAGACACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCACGTGTTCACTGACG 780
Db 751 TCGAGACACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCACGTGTTCACTGACG 810
Qy 781 ACCGCTTTGCCAGATTTGACAGAGGCTTGGGGCGCGCGGAGGCTGCGCGGTGTTGGCC 840
Db 811 ACCGCTTTGCCAGATTTGACAGAGGCTTGGGGCGCGCGGAGGCTGCGCGGTGTTGGCC 870
Qy 841 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGCACTGCTGCTGCTGCTG 900
Db 871 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGCACTGCTGCTGCTGCTG 930
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGCTGAGCAATATCTGCACTC 960
Db 931 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGCTGAGCAATATCTGCACTC 990
Qy 961 CTGCGCTTGAATCTGAGCGGCTACTTCCAAATATGAGGGGTCTGTGACTACACGCGCTGT 1020
Db 991 CTGCGCTTGAATCTGAGCGGCTACTTCCAAATATGAGGGGTCTGTGACTACACGCGCTGT 1050
Qy 1021 GCCCAAGGATGATCTGAGCTGTGTTAAACAGACAGTATCTGAGTCTAAGAGAGCTC 1080
Db 1051 GCCCAAGGATGATCTGAGCTGTGTTAAACAGACAGTATCTGAGTCTAAGAGAGCTC 1110
Qy 1081 CACACCTTCTGAGACACCTGTGAGGAGCTGTGACTCTGCGCTACAGTTAACTTCCGA 1140
Db 1111 CACACCTTCTGAGACACCTGTGAGGAGCTGTGACTCTGCGCTACAGTTAACTTCCGA 1170
Qy 1141 GCGAGCGAGCTTTGAAATGGGAGATGATTGAGGCGCTCTTCCCTGCTGGAATGAGCAGC 1200
Db 1171 GCGAGCGAGCTTTGAAATGGGAGATGATTGAGGCGCTCTTCCCTGCTGGAATGAGCAGC 1230
Qy 1201 AGTCTCTGGGCTGTGAGGCAAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1231 AGTCTCTGGGCTGTGAGGCAAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTG 1290
Qy 1261 GCGCTGTGTTTGGGCTCTCTTTTGTGTGTCACACAGCTGCGTCTCTGTGTGAGATGAGA 1320
Db 1291 GCGCTGTGTTTGGGCTCTCTTTTGTGTGTCACACAGCTGCGTCTCTGTGTGAGATGAGA 1350
Qy 1321 AGGCAAGCAGAGAGGAGAAACAAAGGGGGTGTGAGTACCGCCAGAGAGGTTAGCCGAG 1380
Db 1351 AGGCAAGCAGAGAGGAGAAACAAAGGGGGTGTGAGTACCGCCAGAGAGGTTAGCCGAG 1410
Qy 1381 ACTGAGACCTAGAGGCTGTGATCTTGGAGATGTGAGAGCCAGCCAGAGGACTGTGAGGG 1440
Db 1411 ACTGAGACCTAGAGGCTGTGATCTTGGAGATGTGAGAGCCAGCCAGAGGACTGTGAGGG 1470
Qy 1441 GAGAGCGGTAATGTCCTGCTCCTGCTCANTATGCACTTCTTTTAACTGCAAGAAATTT 1500
Db 1471 GAGAGCGGTAATGTCCTGCTCCTGCTCANTATGCACTTCTTTTAACTGCAAGAAATTT 1530
Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 14
US-10-295-027-305

Sequence 305, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glsh, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
PRIORITY FILING DATE: 2002-11-13
PRIORITY APPLICATION NUMBER: US 09/663,733
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 60/350,666
PRIORITY FILING DATE: 2001-11-13
PRIORITY APPLICATION NUMBER: US 60/335,394
PRIORITY FILING DATE: 2001-11-15
PRIORITY APPLICATION NUMBER: US 60/332,464
PRIORITY FILING DATE: 2001-11-21
PRIORITY APPLICATION NUMBER: US 60/334,393
PRIORITY FILING DATE: 2001-11-29
PRIORITY APPLICATION NUMBER: US 60/340,376
PRIORITY FILING DATE: 2001-12-14
PRIORITY APPLICATION NUMBER: US 60/347,211
PRIORITY FILING DATE: 2002-01-08
PRIORITY APPLICATION NUMBER: US 60/347,349
PRIORITY FILING DATE: 2002-01-10
PRIORITY APPLICATION NUMBER: US 60/355,250
PRIORITY FILING DATE: 2002-02-08
PRIORITY APPLICATION NUMBER: US 60/356,714
PRIORITY FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 305
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-305
Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACAGTCAGCGCAGTGGCTCCCTGTGCCCCAGGCCCTTGAGCTCCCTGTGATCCCGGCC 60
Db 31 ACAGTCAGCGCAGTGGCTCCCTGTGCCCCAGGCCCTTGAGCTCCCTGTGATCCCGGCC 90
Qy 61 CCGTCTCCAGGCTCAGCTGAGCACTGCTGTGTCACCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 91 CCGTCTCCAGGCTCAGCTGAGCACTGCTGTGTCACCTGCTGCTGCTGCTGCTGCTGCTG 150
Qy 121 CCCAGAGGTTGCCCGGAGTCAGAGAGATTTCCCTTGGAGAGGCTCTTCTGGGGA 180
Db 151 CCCAGAGGTTGCCCGGAGTCAGAGAGATTTCCCTTGGAGAGGCTCTTCTGGGGA 210
Qy 181 GATACCCACTGGGCGAGAGATTTCCCAAGTGAAGAGATTCACCCAGAGAGAGAT 240
Db 211 GATACCCACTGGGCGAGAGATTTCCCAAGTGAAGAGATTCACCCAGAGAGAGAT 270
Qy 241 CCAGCCGAGAGAGAGATCTACCTGAGAGAGAGATTTACCTGAGAGAGAGATCTACCT 300
Db 271 CCAGCCGAGAGAGAGATCTACCTGAGAGAGAGATTTACCTGAGAGAGAGATCTACCT 330
Qy 301 GAGTTAAGCTTAATCAAGAGAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGTT 360

Db 331 GAAGTTAAGCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTT 390
Qy 361 GAGGCTCTGAGAGATCTCTAAGAAAGGCTCAAGATATATGCCAGAGGAGCAAGAGAGGAGAT 420
Db 391 GAGGCTCTGAGAGATCTCTAAGAAAGGCTCAAGATATATGCCAGAGGAGCAAGAGAGGAGAT 450
Qy 421 GACAGAGATCATTTGGGCTATGAGAGGAGAGAGGCTCCGCTGAGGCTCCGAGGCTCCGAGCTGC 480
Db 451 GACAGAGATCATTTGGGCTATGAGAGGAGAGAGGCTCCGCTGAGGCTCCGAGGCTCCGAGCTGC 510
Qy 481 GCGGAGCGGCTTCCAGATGTCCTCCGCTGAGATATCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 540
Db 511 GCGGAGCGGCTTCCAGATGTCCTCCGCTGAGATATCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 570
Qy 541 GCGGAGCGGCTTCCAGATGTCCTCCGCTGAGATATCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 600
Db 571 GCGGAGCGGCTTCCAGATGTCCTCCGCTGAGATATCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 630
Qy 601 AACAAATGAGCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTC 660
Db 631 AACAAATGAGCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTC 690
Qy 661 GAGGAGGAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 720
Db 691 GAGGAGGAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 750
Qy 721 TGGGAGCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 780
Db 751 TGGGAGCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 810
Qy 781 ACCGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 840
Db 811 ACCGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 870
Qy 841 GCGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 900
Db 871 GCGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 930
Qy 901 GAAAGAAATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTC 960
Db 931 GAAAGAAATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTC 990
Qy 961 CTGAGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 1020
Db 991 CTGAGCTTTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 1050
Qy 1021 GCCCAGAGGTGTCATGTCAGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1080
Db 1051 GCCCAGAGGTGTCATGTCAGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1110
Qy 1081 CACACCTCTCTGACACCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1111 CACACCTCTCTGACACCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
Qy 1141 GCGAGCAGACCTTTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1171 GCGAGCAGACCTTTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Qy 1201 AGTCTCTGAGAGCTGTCAGAGCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 1260
Db 1231 AGTCTCTGAGAGCTGTCAGAGCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 1290
Qy 1261 GCGCTGAGTTTGGGCTCTCTTTTGGCTGTCACAGAGGTGCGCTTCTTTGTCAGATGAGAA 1320
Db 1291 GCGCTGAGTTTGGGCTCTCTTTTGGCTGTCACAGAGGTGCGCTTCTTTGTCAGATGAGAA 1350
Qy 1321 AGGAGCAGACAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1351 AGGAGCAGACAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
Qy 1381 ACTGAGCTTGAAGGCTGATCTTGGAGAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1411 ACTGAGCTTGAAGGCTGATCTTGGAGAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470

Qy 1441 GGAGCCGGTAACATGTCCTCTGTCCTGTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1500
Db 1471 GAGCCGGTAACATGTCCTCTGTCCTGTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1530
Qy 1501 TTTTAAATTAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAATTAAT 1552

RESULT 15
US-10-295-027-1022
; Sequence 1022, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevizi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of diagnosis of Cancer. Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1022
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1022

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTACGCGCATGAGCTCCCTGTGACCCAGACCCCTGCTCCTGTGATGCCGAGC 60
Db 31 ACAGTACGCGCATGAGCTCCCTGTGACCCAGACCCCTGCTCCTGTGATGCCGAGC 90
Qy 61 CCTGCTCCAGGCTCACTGTGCACTGTCGTGTCATGTCGTGTCATGTCGTGTCATGTCGTGTCATGTCGTGTCAT 120
Db 91 CCTGCTCCAGGCTCACTGTGCACTGTCGTGTCATGTCGTGTCATGTCGTGTCATGTCGTGTCATGTCGTGTCAT 150
Qy 121 CCCAGAGGTTCCCGAGATGAGAGAGATTCCTTGGAGAGAGGCTCTTCTGGAGAA 180

Db 151 CCCAAGGTTGCCCCGAGATGCAAGAGATTCCCCCTTGGAGAGAGCTCTTGGGGAA 210
QY 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGAT 240
Db 211 GATGACCACTGGGCGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGAT 270
QY 241 CCAACCCGAGAGAGAGATCTAAGAGAGAGATCTAAGAGAGAGATCTAAGAT 300
Db 271 CCAACCCGAGAGAGAGATCTAAGAGAGAGATCTAAGAGAGAGATCTAAGAT 330
QY 301 GAAGTTAAGCTTAATCAGAGAAGAGAGCTCCCTGAAGTTAGAGATCTAAGAT 360
Db 331 GAAGTTAAGCTTAATCAGAGAAGAGAGCTCCCTGAAGTTAGAGATCTAAGAT 390
QY 361 GAGGCTCTGAGAGATCTTCAAGAACCCAGAGATTAATGCCCAAGAGAGAGAT 420
Db 391 GAGGCTCTGAGAGATCTTCAAGAACCCAGAGATTAATGCCCAAGAGAGAT 450
QY 421 GACCAAGTCAATGGGGCTATGGAGGCGACCCGCTGGCCCGGGGTGCCAGGCTGC 480
Db 451 GACCAAGTCAATGGGGCTATGGAGGCGACCCGCTGGCCCGGGGTGCCAGGCTGC 510
QY 481 GCGGCGCGCTTCCAGTCCCGGAGATATCCGCGCCAGCTGCGCTTCTGCGCGGC 540
Db 511 GCGGCGCGCTTCCAGTCCCGGAGATATCCGCGCCAGCTGCGCTTCTGCGCGGC 570
QY 541 CTGCGCGCTTCCAGTCTGAGCTTCCAGCTTCCGCGCTTCCAGATCTGCGCTGC 600
Db 571 CTGCGCGCTTCCAGTCTGAGCTTCCAGCTTCCGCGCTTCCAGATCTGCGCTGC 630
QY 601 AACCAATGGCACAGTGTGCACTGACCCGCTGCTGGGCTAGAGATGGCTCTGGTCCC 660
Db 631 AACCAATGGCACAGTGTGCACTGACCCGCTGCTGGGCTAGAGATGGCTCTGGTCCC 690
QY 661 GGGCGGAGATCCGGCTCTGAGCTGATCTGCACTGGGCGGCTGCAAGTGTGCGGC 720
Db 691 GGGCGGAGATCCGGCTCTGAGCTGATCTGCACTGGGCGGCTGCAAGTGTGCGGC 750
QY 721 TGGAGACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCAAGTGTCACTCACT 780
Db 751 TGGAGACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCAAGTGTCACTCACT 810
QY 781 ACCGCTTTCCAGAGTTGACGAGGCTTGGGGCGCCGGGAGGCTGCGCGTGTGGCC 840
Db 811 ACCGCTTTCCAGAGTTGACGAGGCTTGGGGCGCCGGGAGGCTGCGCGTGTGGCC 870
QY 841 GCTTTTCTGAGAGAGGCGCCGGAAGAAAAGTGTCTATGACAGTGTCTGCTTG 900
Db 871 GCTTTTCTGAGAGAGGCGCCGGAAGAAAAGTGTCTATGACAGTGTCTGCTTG 930
QY 901 GAAAGAAATGGCTGAGAGAGGCTCAGAGATCAAGTGTCCAGAGCTGACATATCTGACTC 960
Db 931 GAAAGAAATGGCTGAGAGAGGCTCAGAGATCAAGTGTCCAGAGCTGACATATCTGACTC 990
QY 961 CTGCGCTTGAAGCTTGAAGCGCTACTTCAATATGAGGGGTCTGTGACTACACCGCTGT 1020
Db 991 CTGCGCTTGAAGCTTGAAGCGCTACTTCAATATGAGGGGTCTGTGACTACACCGCTGT 1050
QY 1021 GCCCAGGCTGATCTGATCTGTGTTTAAACAGACAGTATGCTGATGCTAAGCAGCTC 1080
Db 1051 GCCCAGGCTGATCTGATCTGTGTTTAAACAGACAGTATGCTGATGCTAAGCAGCTC 1110
QY 1081 CACACCTCTCTGACACCTCTGAGGAGCTGTGATCTCTGCGCTACAGTGAATCTTCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGAGGAGCTGTGATCTCTGCGCTACAGTGAATCTTCCGA 1170
QY 1141 GCGAGCAGCCTTTGAATGGGCGAGTATGAGGCTCTTCCCTGCTGAGTGAAGCAGC 1200
Db 1171 GCGAGCAGCCTTTGAATGGGCGAGTATGAGGCTCTTCCCTGCTGAGTGAAGCAGC 1230
QY 1201 AGTCTCTGGGCTGTGAGGCAAGTCAAGTGAATTCCTGCTGGCTGTGAGCAATCTTA 1260
Db 1231 AGTCTCTGGGCTGTGAGGCAAGTCAAGTGAATTCCTGCTGGCTGTGAGCAATCTTA 1290

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Search completed: February 6, 2005, 11:25:27
Job time : 868 secs

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OY	121	CCCCAGAGGTTGCCCCCGAGTCAGAGGATTTCCCTCTTGGAGAGAGCTCTTCTGTGGGAA	180
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OY	181	GATGACCCACTGGGGAGAGGAGATCTMGCCCACTGAAAGAGATTTCAACCAAGAGAGGAGAT	240
Db	210	GATGACCCACTGGGGAGAGGAGATCTGCCCACTGAAAGAGATTTCAACCAAGAGAGGAGAT	269
OY	241	CCACCCCGAGAGAGAGATCTTACTGTAGAGAGAGATTTACTCTGTAGAGAGAGATTTACTT	300
Db	270	CCACCCCGAGAGAGAGATTTACTGTAGAGAGAGATTTACTCTGTAGAGAGAGATTTACTT	329
OY	301	GAACTTAAAGCTTAAATTCAGAAAGAGAGGCTCCCTGAAAGTTAGAGATTTACTTCTGT	360
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OY	361	GAGGCTCTGAGAGATCTCTAAGAAACCCCAAGATTAATGCCACAGGGAACAAAGAGAGAT	420
Db	390	GAGGCTCTGAGAGATCTCTAAGAAACCCCAAGATTAATGCCACAGGGAACAAAGAGAGAT	449
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Db	450	GACCAAGTCATTGGCGCTATAGAGAGCGACCCGCTCTGGCCCCGAGTGTCCCAAGCTTGC	509
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Db	510	GCGGGCGGCTTCAATGCCCGGTGATATTCGCGCCCAAGCTGCGCGCTTCTGCGCGGCG	569
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Db	570	CTGCGCGCCCTGGAATCTCTGGGCTTCCAGACTCCGCGGCTCCAGAACTGCGCGCTGCG	629
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OY	661	GGGCGGAGATACCGGAGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTGTCCGAGC	720
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Db	1530	TTTTAAATATAA 1541	
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LOCUS			
DEFINITION	CR620502	1523 bp	mRNA
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			full-length cDNA clone CS0DK007YK10 of Hela cells Cot 25-normalized
			of Homo sapiens (human).
ACCESSION	CR620502		
VERSION	CR620502.1	GI:50501309	
KEYWORDS	HTC; CNSLT cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1523)		
AUTHORS	L.I.W.B., Gruber,C., Jesse,J. and Polayer,D.		
FILE	L.I.W.B., Gruber,C., Jesse,J. and Polayer,D.		
JOURNAL	Full-length cDNA libraries and normalization		
REMARK	Unpublished		
	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
	Parade Avenue		
REFERENCE	2 (bases 1 to 1523)		
AUTHORS	Genoscope.		
FILE	Genoscope.		
JOURNAL	Direct Submission		
	Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen.		
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 1520 TTTT 1523

RESULT 3
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 ACCESSION
 CRE16345
 VERSION
 CRE16345.1 GI:50497152
 KEYWORDS
 HTC; CNSLT_cDNA.
 SOURCE
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 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 (bases 1 to 1469)
 Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact : Peng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1469)
 REFERENCE
 Genoscope.
 Direct Submission
 Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and BclI V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION AL558378
VERSION AL558378.3 GI:46183776
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1009)
AUTHORS Li, W.B., Gruber, C., Desse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31280177.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DJ005PF07QPlc=5300.f.
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QY	721	TCGAGACACACTGTGGAAGAGCCACCGTTCCCTGCGAGATCAAGTGTTCACCTCAGC	780
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QY	781	ACCGGCTTTCGCAAGTTGACGAGGCTTTGGGCGCCCGGAGGCGCTTGCGTGTGGC	839
Db	811	ACCGGCTTTCGCAAGTTGACGAGGCGCTTTGGGCGCCCGGAGGCGCTTGCGTGTGGC	869

division of Invitrogen.
 This sequence belongs to sequence cluster 8734.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DB010CA10QP2&c=8734.f>
 location/Qualifiers
 1..1084

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YB19"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five primed and enriched
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

```

Query Match	825;	DB 1;	length 1084;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 925;	Conservative 0;	Mismatches 2;	Indels 0;
			Gaps 0

[illegible]

QY 421 GACCAAGTCAATTGGCGCTATGAGGCGACCCGCGCTGCGCGGCTGTCCCAAGCTTCG 480
DB 450 GACCAAGTCAATTGGCGCTATGAGGCGACCCGCGCTGCGCGGCTGTCCCAAGCTTCG 509
QY 481 GGGGGCGCTTCCAGTCCCGGCTGATATCCCGCCCACTGCGCGCTTTCGCGCGCC 540
DB 510 GGGGGCGCTTCCAGTCCCGGCTGATATCCCGCCCACTGCGCGCTTTCGCGCGCC 569
QY 541 CTGGCGCCCTGGAAGTCTCTGGGCTTCCAGTCCCGCGCTGCGCGGCTGCGCGGCG 600
DB 570 CTGGCGCCCTGGAAGTCTCTGGGCTTCCAGTCCCGCGCTGCGCGGCTGCGCGGCG 629
QY 601 AACAAATGCGACAGTGTGCACTGACCTGCTCTGCGCTAGAGATGCGCTGAGTCCG 660
DB 630 AACAAATGCGACAGTGTGCACTGACCTGCTCTGCGCTAGAGATGCGCTGAGTCCG 689
QY 661 GGGCGCGGAGT 670
DB 690 GGGCGCGGAGT 699

RESULT 10
BG386425 874 bp mRNA linear EST 12-MAR-2001
LOCUS 602455652P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583869 5',
DEFINITION mRNA sequence.
ACCESSION BG386425
VERSION BG386425.1 GI:13279871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgepbrs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1308 row: h column: 14
High quality sequence stop: 714.
Location/Qualifiers
1. 874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4583869"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGCG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 40.5%; Score 617; DB 4; Length 874;
Best Local Similarity 100.0%; Pred. No. 3.7e-305; Indels 0; Gaps 0;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
207 GCCAATGGAAGATTCACCAAGAGAGAGATCCACCGGAGAGAGATCTACTGG 266
|||||

DB 1 GCCAATGGAAGATTCACCAAGAGAGAGATCCACCGGAGAGAGATCTACTGG 60
QY 267 AGAGAGAGATCTACTGAGAGAGAGATCTACTGAGATTAAGCTTAATCAGAGAGA 326
DB 61 AGAGAGAGATCTACTGAGAGAGAGATCTACTGAGATTAAGCTTAATCAGAGAGA 120
QY 327 GGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTGAGATCTCAAGAAC 386
DB 121 GGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTGAGATCTCAAGAAC 180
QY 387 CCAAGATTAATGCCACAGGAGCAAGAGAGAGATGACAGAGTCAATGGCGCTATGAGAG 446
DB 181 CCAAGATTAATGCCACAGGAGCAAGAGAGAGATGACAGAGTCAATGGCGCTATGAGAG 240
QY 447 CGAACCGCGCTGAGCGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 506
DB 241 CGAACCGCGCTGAGCGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 300
QY 507 TATCGCGCCCGAGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 566
DB 301 TATCGCGCCCGAGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 360
QY 567 CGAGCTCCCGCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 626
DB 361 CGAGCTCCCGCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 420
QY 627 CCGTGCCTCTGGGCTGAGAGATGAGTCTGCTGCGCGGCTGCGCGGCTGCGCGGCTG 686
DB 421 CCGTGCCTCTGGGCTGAGAGATGAGTCTGCTGCGCGGCTGCGCGGCTGCGCGGCTG 480
QY 687 GCATCTGCACTGGGGGCTGCAAGTCTGCGGCTGCGAGCACTGTGGAAGCCACCG 746
DB 481 GCATCTGCACTGGGGGCTGCAAGTCTGCGGCTGCGAGCACTGTGGAAGCCACCG 540
QY 747 TTTCCTGCGAGATTCACGTGCTTCACTGACACCGCTTTGCCAGATTGACGAGC 806
DB 541 TTTCCTGCGAGATTCACGTGCTTCACTGACACCGCTTTGCCAGATTGACGAGC 600
QY 807 CTTGGGGGCGCGCGGAG 823
DB 601 CTTGGGGGCGCGCGGAG 617

RESULT 11
A1925646/c 669 bp mRNA linear EST 08-MAR-2000
LOCUS w032d07.x1 NCI_CGAP Gas4 Homo sapiens cDNA clone IMAGE:2457037 3',
DEFINITION similar to TR:Q16790 Q16790 CARBONIC ANHYDRASE ;, mRNA sequence.
ACCESSION A1925646
VERSION A1925646.1 GI:5661536
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 669)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgepbrs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LNL at:
http://www-bio.llnl.gov/bbtp/image/image.html
Insert length: 819 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 416.

FEATURES
SOURCE

Location/Qualifiers
1. .669
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image:2457037"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11349-011"

ORIGIN

Query Match 36.5%; Score 555; DB 1; Length 669;
Best Local Similarity 99.8%; Pred. No. 2.7e-273;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

917 AAGGCTCAGAGACTGAGTCCAGAGACTGACATATCTGACTCTGCTCTGACTTCA 976
DB AAGGCTCAGAGACTGAGTCCAGAGACTGACATATCTGACTCTGCTCTGACTTCA 547
977 GCGGCTACTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCGGAGGTTCATCT 1036
DB GCGGCTACTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCGGAGGTTCATCT 487
546 GCGGCTACTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCGGAGGTTCATCT 487
9137 GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 1096
DB GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 427
466 GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 427
9137 GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 1156
DB GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 367
426 GGAAGTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTCCACACCTCTCTGACA 367
1157 ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 1216
DB ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 307
366 ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 307
1217 AGCGAGTCAGAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1276
DB AGCGAGTCAGAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
306 AGCGAGTCAGAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
9137 ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 1336
DB ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 187
246 ATGGGCGAATGATTGAGGCTCTCTGCTGCTGAGTGAACGAGTCTCTGGGCTGCTG 187
1337 GAAACCAAGGGGGTGTGAGTACCGCCGACAGAGAGTGAAGCTGAGAGCTTGAAGGC 1396
DB GAAACCAAGGGGGTGTGAGTACCGCCGACAGAGAGTGAAGCTGAGAGCTTGAAGGC 127
1397 TGGATCTTGAAGATGTGAGAACGACGACAGAGCTGAGAGGGGAGCGGTTAACTGTC 1456
DB TGGATCTTGAAGATGTGAGAACGACGACAGAGCTGAGAGGGGAGCGGTTAACTGTC 67
126 TGGATCTTGAAGATGTGAGAACGACGACAGAGCTGAGAGGGGAGCGGTTAACTGTC 67
9137 TGGATCTTGAAGATGTGAGAACGACGACAGAGCTGAGAGGGGAGCGGTTAACTGTC 1516
DB TGGATCTTGAAGATGTGAGAACGACGACAGAGCTGAGAGGGGAGCGGTTAACTGTC 7
1517 TATTAAT 1522
DB TATTAAT 1
6 TATTAAT 1

RESULT 12
CA425935/6 689 bp mRNA linear EST 07-NOV-2002

LOCUS CA425935 UI-H-FBI-beg-j-10-0-UI.61 NCI CGAP FBI Homo sapiens cDNA clone

DEFINITION UI-H-FBI-beg-j-10-0-UI 3', mRNA sequence.
ACCESSION CA425935
VERSION CA425935.1 GI:24788661
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 689)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-42, >AT rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

SOURCE

Location/Qualifiers
1. .689
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FBI-beg-j-10-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FBI"
/note="Organ: Chondrosarcoma; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FBI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares.
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGTACGAGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG Tissue=Human grade 2 chondrosarcoma cell line pool
TAG Lib=UI-H-FBI
TAG_SEQ=CGCTACGAGAC"

ORIGIN

Query Match 36.5%; Score 555; DB 6; Length 689;
Best Local Similarity 99.7%; Pred. No. 2.7e-273;
Matches 655; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

849 GAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTCCTGCTGCTGGAAGAAT 908
DB GAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTCCTGCTGCTGGAAGAAT 630
689 GAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTCCTGCTGCTGGAAGAAT 630
909 GCGTGAAGAGGCTCAGAGCTCAGAGTCCAGAGCTGACATATGAGCTCTGAGCCCTC 968
DB GCGTGAAGAGGCTCAGAGCTCAGAGTCCAGAGCTGACATATGAGCTCTGAGCCCTC 570
629 GCGTGAAGAGGCTCAGAGCTCAGAGTCCAGAGCTGACATATGAGCTCTGAGCCCTC 570
969 TGACTTCAGCCGCTACTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGGG 1028
DB TGACTTCAGCCGCTACTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGGG 510
1029 TGTCACTGAGACTGTGTTTAAACAGACAGTATGCTGAGTGTGTAAGAGCTTCAACCTT 1088
DB TGTCACTGAGACTGTGTTTAAACAGACAGTATGCTGAGTGTGTAAGAGCTTCAACCTT 450
509 TGTCACTGAGACTGTGTTTAAACAGACAGTATGCTGAGTGTGTAAGAGCTTCAACCTT 450
9137 CTCTGACACCTGTGGGAGCTGTGGTGAAGCTTCGCTACAGCTGAACCTTCCAGAGCAGCA 1148

Db 449 CTCGACACCCCTGGGAGCCTGTGACTCTCGGCTACAGCTGAACCTCCGAGCAGCA 390
 1149 GCGTTTGAATGGCCGAGTATTTAGAGCCTCTTCCCTGCTGAGTGAACAGCAGTCTCG 1208
 Db 389 GCGTTTGAATGGCCGAGTATTTAGAGCCTCTTCCCTGCTGAGTGAACAGCAGTCTCG 330
 1209 GCGTGTGAGCAGTCAAGCTGAATTCCTGCTGAGTGAATTCCTGAGTGAATTCCTGAGT 1268
 Db 329 GCGTGTGAGCAGTCAAGCTGAATTCCTGCTGAGTGAATTCCTGAGTGAATTCCTGAGT 270
 1269 TTTTGGCTCTTTTGTGTGTCAACAGCCTGCGCTTCTTGTGCAATGAGAGAGCA 1328
 Db 269 TTTTGGCTCTTTTGTGTGTCAACAGCCTGCGCTTCTTGTGCAATGAGAGAGCA 210
 1329 CAGAGGGGAAACCAAGGGGGGTGTGAGTACCGCCCAAGCAGAGTGAAGCAGTGAAGC 1388
 Db 209 CAGAGGGGAAACCAAGGGGGGTGTGAGTACCGCCCAAGCAGAGTGAAGCAGTGAAGC 150
 1389 CTAGAGGCTGATCTTGAAGATGTGAGAGCAGAGCAGAGCAGTGAAGGGGAGCGG 1448
 Db 149 CTAGAGGCTGATCTTGAAGATGTGAGAGCAGAGCAGAGCAGTGAAGGGGAGCGG 90
 1449 TAAGTCTCTGCTGCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATTTTAA 1505
 Db 89 TAAGTCTCTGCTGCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATTTTAA 33

RESULT 13
 BM552941 627 bp mRNA linear EST 20-FEB-2002
 LOCUS BM552941
 DEFINITION AGENCOURT_6542619 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742739
 5', mRNA sequence.
 ACCESSION BM552941 GI:18791234
 VERSION BM552941.1
 KEYWORDS Homo sapiens (human)
 SOURCE EST.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strauberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: L14M12761 row: f column: 20
 High quality sequence stop: 599.
 Location/Qualifiers
 1..627
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742739"
 /rname_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES
 source

ORIGIN

Query Match 34.9%; Score 531; DB 4; Length 627;

Best Local Similarity 100.0%; Pred.No.5.9e-261; Mismatches 0; Indels 0; Gaps 0;

Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

990 ATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGAGGTGTCATGTGATGTTAA 1049
 Db 52 ATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGAGGTGTCATGTGATGTTAA 111
 1050 CCAGACAGTATGCTGATGCTTAAGCAGCTCCACACCTCTGTGACACCTGTGGGAGC 1109
 Db 112 CCAGACAGTATGCTGATGCTTAAGCAGCTCCACACCTCTGTGACACCTGTGGGAGC 171
 1110 TGGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1169
 Db 172 TGGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 231
 1170 TGAAGCCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
 Db 232 TGAAGCCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
 1230 GAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1289
 Db 292 GAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
 1290 CACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
 Db 352 CACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
 1350 TGTGAGCTACCGCCGAGAGGAGTACCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1409
 Db 412 TGTGAGCTACCGCCGAGAGGAGTACCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 471
 1410 ATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1469
 Db 472 ATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 531
 1470 TATGCCACTTCTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1520
 Db 532 TATGCCACTTCTTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582

RESULT 14
 CA416326/c 659 bp mRNA linear EST 07-NOV-2002
 LOCUS CA416326
 DEFINITION UI-H-FBO-dbu-1-22-0-UI.81 NCI CGAP FBO Homo sapiens cDNA clone
 UI-H-FBO-dbu-1-22-0-UI 3', mRNA sequence.
 ACCESSION CA416326
 VERSION CA416326.1 GI:24778977
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strauberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: James Martin
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 1-42, >AT-richFlow_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.
 Location/Qualifiers

FEATURES

source
1. 659
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FEO-bpu-1-22-0-UI"
/tissue_type="Chondrosarcoma Cell line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/lab_lib="NCI CGAP FEO"
/note="Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FEO is a cDNA library containing the following tleses): a pool of 3 chondrosarcoma cell lines (grade 2) The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCTACGAC. The cell lines was provided by Dr James Martin of University of Iowa.
TAG LIB=UI-H-FEO
TAG_SEQ=CGCTACGAC"

ORIGIN

Query Match 34.6%; Score 526; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 2.2e-258;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 997 GGGTCTGACTACACCGCCCTGTCAGAGGTGATCTGATGATGTTTAAACAGACA 1056
DB 541 GGGTCTGACTACACCGCCCTGTCAGAGGTGATCTGATGATGTTTAAACAGACA 482
QY 1057 GTGAGCTGAGTCTAAGACAGTCTCCACCCCTCTGACACCTCTGAGGAGCTGTGTAC 1116
DB 481 GTGAGCTGAGTCTAAGACAGTCTCCACCCCTCTGACACCTCTGAGGAGCTGTGTAC 422
QY 1117 TCTGCGCTACAGTGAATCTCCAGAGGAGCAGCTTGAATGAGGAGTGAAGGCGC 1176
DB 421 TCTGCGCTACAGTGAATCTCCAGAGGAGCAGCTTGAATGAGGAGTGAAGGCGC 362
QY 1177 TCTTCTCTGCTGAGTGAACAGAGTCTCTGAGGCTGTCAGCAGTCACTGAATTCC 1236
DB 361 TCTTCTCTGCTGAGTGAACAGAGTCTCTGAGGCTGTCAGCAGTCACTGAATTCC 302
QY 1237 TGGCTGCTGCTGAGTGAACATCTAGCCCTGTTTGGCTCTCTTTGCTGACACAGC 1296
DB 301 TGGCTGCTGCTGAGTGAACATCTAGCCCTGTTTGGCTCTCTTTGCTGACACAGC 242
QY 1297 GTGCGCTCTCTGAGTGAACAGAGCAGACAGAGGAGGAAACAAAGGGGTGTAGC 1356
DB 241 GTGCGCTCTCTGAGTGAACAGAGCAGACAGAGGAGGAAACAAAGGGGTGTAGC 182
QY 1357 TACCGCCAGCAGAGTGAACAGAGTGAAGCTTGAAGCTTGAAGTGTAGG 1416
DB 181 TACCGCCAGCAGAGTGAACAGAGTGAAGCTTGAAGCTTGAAGTGTAGG 122
QY 1417 AAGCCAGCAGAGGAGTGAAGGAGGAGCGGTAATGTCGTCGTCATTATGCA 1476
DB 121 AAGCCAGCAGAGGAGTGAAGGAGGAGCGGTAATGTCGTCGTCATTATGCA 62
QY 1477 CTTCCTTTTAACTGCAAGAAATTTTAAATATTTATTAAT 1522
DB 61 CTTCCTTTTAACTGCAAGAAATTTTAAATATTTATTAAT 16

RESULT 15
A1831707/c A1831707 682 bp mRNA linear EST 21-DEC-1999
LOCUS

DEFINITION
w40h01.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2405329 3', similar to TR:Q16790 Q16790 CARBONIC ANHYDRASE 1, mRNA sequence.
A1831707
ACCESSION
VERSION
A1831707.1 GI:5452464
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 682)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMW at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 1322 Std Error: 0.00
Seq primer: -400P from G1bco
High quality sequence stop: 424.
Location/Qualifiers
1. 682
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:2405329"
/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu19"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

Query Match 33.8%; Score 514; DB 1; Length 682;
Best Local Similarity 99.7%; Pred. No. 3.2e-252;
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 997 ATCGGTGAGAGGCTGAGAGTCCAGGCTCCAGAGTGAACATCTGCACTCTGCGC 966
DB 616 ATCGGTGAGAGGCTGAGAGTCCAGGCTCCAGAGTGAACATCTGCACTCTGCGC 557
QY 967 TCTGACTACCGCTACTTCCATATGAGGAGTCTGACTACACCGCCCTGTGCCAG 1026
DB 556 TCTGACTACCGCTACTTCCATATGAGGAGTCTGACTACACCGCCCTGTGCCAG 497
QY 1027 GGTGTCATCTGAGTGTGTTTAAACAGAGTATGCTGATGCTTAAAGACTCCAGC 1086
DB 496 GGTGTCATCTGAGTGTGTTTAAACAGAGTATGCTGATGCTTAAAGACTCCAGC 437
QY 1087 CTCTGAGACCCCTGTGGGAGCTGTGATCTCTGAGCTGAAGCTTCCAGCGAGC 1146
DB 436 CTCTGAGACCCCTGTGGGAGCTGTGATCTCTGAGCTGAAGCTTCCAGCGAGC 377
QY 1147 CAGCTTTGAATGGGCGAGTATGAGGCTCTCTCTGCTGAGTGAAGCAGAGTCT 1206
DB 376 CAGCTTTGAATGGGCGAGTATGAGGCTCTCTCTGCTGAGTGAAGCAGAGTCT 317

ORIGIN

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Qy 1207 CGGGCTGTGAGCCAGTCCAGTGAATTCCTGCTGGCTGTGAGCATCTAGCCCTG 1266
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Db 316 CGGGCTGTGAGCCAGTCCAGTGAATTCCTGCTGGCTGTGAGCATCTAGCCCTG 257
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Qy 1267 GTTTTGGCTCTCTTTTGTGTCAACAGCGTCGCGTTCCTGTGCAGATGAGAAAGCAG 1326
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Search completed: February 6, 2005, 10:50:07
 Job time : 4455 secs

Blank (uspio)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2005, 23:23:52 ; Search time 6352 Seconds
(without alignments) 11331.065 Million cell updates/sec

Title: US-09-967-237A-1

Perfect score: 1522

Sequence: 1 acagcgcagccgcatgctcc.....ttaataataattataat 1522

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_ov:*

7: gb_ov:*

8: gb_ov:*

9: gb_ov:*

10: gb_ov:*

11: gb_ov:*

12: gb_ov:*

13: gb_ov:*

14: gb_ov:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1522	100.0	1522	6 AR074439	Sequence
2	1522	100.0	1522	6 AR081119	Sequence
3	1522	100.0	1522	6 AR085316	Sequence
4	1522	100.0	1522	6 AR088064	Sequence
5	1522	100.0	1522	6 AR104223	Sequence
6	1522	100.0	1522	6 AR143487	Sequence
7	1522	100.0	1522	6 AR171392	Sequence
8	1522	100.0	1522	6 AR171563	Sequence
9	1522	100.0	1522	6 BD243152	MN gene a
10	1522	100.0	1522	6 CQ834035	Sequence
11	1522	100.0	1522	6 AX330007	Sequence
12	1522	100.0	1522	6 AX332607	Sequence
13	1522	100.0	1522	6 AX333244	Sequence
14	1522	100.0	1522	6 AX336174	Sequence
15	1522	100.0	1522	6 HSMATDWN	Sequence
16	1520.4	99.9	1519	9 BC014950	Homo sapi
17	1517.4	91.9	1399	6 AR095263	Sequence
18	1399	82.0	1289	6 CQ726696	Sequence
19	1247.4				

20	759.2	49.9	1965	10 MMU245857	AJ245857 Mus muscu
21	457.8	30.1	1671	10 AB086322	AB086322 Mus muscu
22	414.4	27.2	6521	6 CO806582	CO806582 Sequence
23	414.4	27.2	6521	6 AX795690	AX795690 Sequence
24	414.4	27.2	6521	6 AX822141	AX822141 Sequence
25	414.4	27.2	6521	6 AX825781	AX825781 Sequence
26	414.4	27.2	10898	6 AR074442	AR074442 Sequence
27	414.4	27.2	10898	6 AR081122	AR081122 Sequence
28	414.4	27.2	10898	6 AR085319	AR085319 Sequence
29	414.4	27.2	10898	6 AR088067	AR088067 Sequence
30	414.4	27.2	10898	6 AR104226	AR104226 Sequence
31	414.4	27.2	10898	6 AR143490	AR143490 Sequence
32	414.4	27.2	10898	6 AR171395	AR171395 Sequence
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36	414.4	27.2	187856	9 AF334829	AF334829 Homo sapi
37	413.4	27.2	415	6 AR074454	AR074454 Sequence
38	413.4	27.2	415	6 AR081134	AR081134 Sequence
39	413.4	27.2	415	6 AR085331	AR085331 Sequence
40	413.4	27.2	415	6 AR088079	AR088079 Sequence
41	413.4	27.2	415	6 AR104238	AR104238 Sequence
42	413.4	27.2	415	6 AR143502	AR143502 Sequence
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DEFINITION	AR074439				
ACCESSION	AR074439				
VERSION	AR074439.1	GI:10001194			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1522)				
AUTHORS	Zavada,J., Pastorekova,S. and Pastorek,J.				
TITLE	Method of inhibiting tumor growth using antibodies to MN protein				
JOURNAL	Patent: US 5955075-A 1 21-Sep-1999;				
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DEFINITION AR081119
ACCESSION AR081119
VERSION AR081119.1 GI:10007847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
Zavada, J., Pastorekova, S. and Pastorek, J.
AUTHORS MN proteins, polypeptides, fusion proteins and fusion polypeptides
TITLE Patent: US 5972353-A 1 26-OCT-1999;
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Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 421 GACAGAGTCAATGCGCTATGAGAGGCAACCGCTGAGCCCGAGGTGCCCAAGCTGC 480
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Chr	Start (kb)	End (kb)	Gene	Transcript	Length (bp)	GC (%)	GC3 (%)	GC3+ (%)	GC4 (%)	GC4+ (%)	GC5 (%)	GC5+ (%)	GC6 (%)	GC6+ (%)	GC7 (%)	GC7+ (%)	GC8 (%)	GC8+ (%)	GC9 (%)	GC9+ (%)	GC10 (%)	GC10+ (%)	GC11 (%)	GC11+ (%)	GC12 (%)	GC12+ (%)	GC13 (%)	GC13+ (%)	GC14 (%)	GC14+ (%)	GC15 (%)	GC15+ (%)	GC16 (%)	GC16+ (%)	GC17 (%)	GC17+ (%)	GC18 (%)	GC18+ (%)	GC19 (%)	GC19+ (%)	GC20 (%)	GC20+ (%)	GC21 (%)	GC21+ (%)	GC22 (%)	GC22+ (%)	GC23 (%)	GC23+ (%)	GC24 (%)	GC24+ (%)	GC25 (%)	GC25+ (%)	GC26 (%)	GC26+ (%)	GC27 (%)	GC27+ (%)	GC28 (%)	GC28+ (%)	GC29 (%)	GC29+ (%)	GC30 (%)	GC30+ (%)	GC31 (%)	GC31+ (%)	GC32 (%)	GC32+ (%)	GC33 (%)	GC33+ (%)	GC34 (%)	GC34+ (%)	GC35 (%)	GC35+ (%)	GC36 (%)	GC36+ (%)	GC37 (%)	GC37+ (%)	GC38 (%)	GC38+ (%)	GC39 (%)	GC39+ (%)	GC40 (%)	GC40+ (%)	GC41 (%)	GC41+ (%)	GC42 (%)	GC42+ (%)	GC43 (%)	GC43+ (%)	GC44 (%)	GC44+ (%)	GC45 (%)	GC45+ (%)	GC46 (%)	GC46+ (%)	GC47 (%)	GC47+ (%)	GC48 (%)	GC48+ (%)	GC49 (%)	GC49+ (%)	GC50 (%)	GC50+ (%)	GC51 (%)	GC51+ (%)	GC52 (%)	GC52+ (%)	GC53 (%)	GC53+ (%)	GC54 (%)	GC54+ (%)	GC55 (%)	GC55+ (%)	GC56 (%)	GC56+ (%)	GC57 (%)	GC57+ (%)	GC58 (%)	GC58+ (%)	GC59 (%)	GC59+ (%)	GC60 (%)	GC60+ (%)	GC61 (%)	GC61+ (%)	GC62 (%)	GC62+ (%)	GC63 (%)	GC63+ (%)	GC64 (%)	GC64+ (%)	GC65 (%)	GC65+ (%)	GC66 (%)	GC66+ (%)	GC67 (%)	GC67+ (%)	GC68 (%)	GC68+ (%)	GC69 (%)	GC69+ (%)	GC70 (%)	GC70+ (%)	GC71 (%)	GC71+ (%)	GC72 (%)	GC72+ (%)	GC73 (%)	GC73+ (%)	GC74 (%)	GC74+ (%)	GC75 (%)	GC75+ (%)	GC76 (%)	GC76+ (%)	GC77 (%)	GC77+ (%)	GC78 (%)	GC78+ (%)	GC79 (%)	GC79+ (%)	GC80 (%)	GC80+ (%)	GC81 (%)	GC81+ (%)	GC82 (%)	GC82+ (%)	GC83 (%)	GC83+ (%)	GC84 (%)	GC84+ (%)	GC85 (%)	GC85+ (%)	GC86 (%)	GC86+ (%)	GC87 (%)	GC87+ (%)	GC88 (%)	GC88+ (%)	GC89 (%)	GC89+ (%)	GC90 (%)	GC90+ (%)	GC91 (%)	GC91+ (%)	GC92 (%)	GC92+ (%)	GC93 (%)	GC93+ (%)	GC94 (%)	GC94+ (%)	GC95 (%)	GC95+ (%)	GC96 (%)	GC96+ (%)	GC97 (%)	GC97+ (%)	GC98 (%)	GC98+ (%)	GC99 (%)	GC99+ (%)	GC100 (%)	GC100+ (%)	GC101 (%)	GC101+ (%)	GC102 (%)	GC102+ (%)	GC103 (%)	GC103+ (%)	GC104 (%)	GC104+ (%)	GC105 (%)	GC105+ (%)	GC106 (%)	GC106+ (%)	GC107 (%)	GC107+ (%)	GC108 (%)	GC108+ (%)	GC109 (%)	GC109+ (%)	GC110 (%)	GC110+ (%)	GC111 (%)	GC111+ (%)	GC112 (%)	GC112+ (%)	GC113 (%)	GC113+ (%)	GC114 (%)	GC114+ (%)	GC115 (%)	GC115+ (%)	GC116 (%)	GC116+ (%)	GC117 (%)	GC117+ (%)	GC118 (%)	GC118+ (%)	GC119 (%)	GC119+ (%)	GC120 (%)	GC120+ (%)	GC121 (%)	GC121+ (%)	GC122 (%)	GC122+ (%)	GC123 (%)	GC123+ (%)	GC124 (%)	GC124+ (%)	GC125 (%)	GC125+ (%)	GC126 (%)	GC126+ (%)	GC127 (%)	GC127+ (%)	GC128 (%)	GC128+ (%)	GC129 (%)	GC129+ (%)	GC130 (%)	GC130+ (%)	GC131 (%)	GC131+ (%)	GC132 (%)	GC132+ (%)	GC133 (%)	GC133+ (%)	GC134 (%)	GC134+ (%)	GC135 (%)	GC135+ (%)	GC136 (%)	GC136+ (%)	GC137 (%)	GC137+ (%)	GC138 (%)	GC138+ (%)	GC139 (%)	GC139+ (%)	GC140 (%)	GC140+ (%)	GC141 (%)	GC141+ (%)	GC142 (%)	GC142+ (%)	GC143 (%)	GC143+ (%)	GC144 (%)	GC144+ (%)	GC145 (%)	GC145+ (%)	GC146 (%)	GC146+ (%)	GC147 (%)	GC147+ (%)	GC148 (%)	GC148+ (%)	GC149 (%)	GC149+ (%)	GC150 (%)	GC150+ (%)	GC151 (%)	GC151+ (%)	GC152 (%)	GC152+ (%)	GC153 (%)	GC153+ (%)	GC154 (%)	GC154+ (%)	GC155 (%)	GC155+ (%)	GC156 (%)	GC156+ (%)	GC157 (%)	GC157+ (%)	GC158 (%)	GC158+ (%)	GC159 (%)	GC159+ (%)	GC160 (%)	GC160+ (%)	GC161 (%)	GC161+ (%)	GC162 (%)	GC162+ (%)	GC163 (%)	GC163+ (%)	GC164 (%)	GC164+ (%)	GC165 (%)	GC165+ (%)	GC166 (%)	GC166+ (%)	GC167 (%)	GC167+ (%)	GC168 (%)	GC168+ (%)	GC169 (%)	GC169+ (%)	GC170 (%)	GC170+ (%)	GC171 (%)	GC171+ (%)	GC172 (%)	GC172+ (%)	GC173 (%)	GC173+ (%)	GC174 (%)	GC174+ (%)	GC175 (%)	GC175+ (%)	GC176 (%)	GC176+ (%)	GC177 (%)	GC177+ (%)	GC178 (%)	GC178+ (%)	GC179 (%)	GC179+ (%)	GC180 (%)	GC180+ (%)	GC181 (%)	GC181+ (%)	GC182 (%)	GC182+ (%)	GC183 (%)	GC183+ (%)	GC184 (%)	GC184+ (%)	GC185 (%)	GC185+ (%)	GC186 (%)	GC186+ (%)	GC187 (%)	GC187+ (%)	GC188 (%)	GC188+ (%)	GC189 (%)	GC189+ (%)	GC190 (%)	GC190+ (%)	GC191 (%)	GC191+ (%)	GC192 (%)	GC192+ (%)	GC193 (%)	GC193+ (%)	GC194 (%)	GC194+ (%)	GC195 (%)	GC195+ (%)	GC196 (%)	GC196+ (%)	GC197 (%)	GC197+ (%)	GC198 (%)	GC198+ (%)	GC199 (%)	GC199+ (%)	GC200 (%)	GC200+ (%)	GC201 (%)	GC201+ (%)	GC202 (%)	GC202+ (%)	GC203 (%)	GC203+ (%)	GC204 (%)	GC204+ (%)
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DEFINITION      Sequence 1 from patent US 5981711.
ACCESSION       AR085316
VERSION         AR085316.1  GI:10012085
KEYWORDS
SOURCE
ORGANISM        Unknown.
                Unclassified.
REFERENCE       1 (bases 1 to 1522)
AUTHORS        Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE          MN-specific antibodies and hybridomas
JOURNAL        Patent: US 5981711-A 1 09-NOV-1999;
FEATURES
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ORIGIN

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Best Local Similarity		100.0%;	Prod. No. 1.6e-310;		
Matches 1522;	Conservative	0;	Mismatches	0;	Indels
					Gaps 0;
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QY	61	CTTCTCTCAGGCTCTCATCTGTGCAACTGTGTGTGTCACTGTGTCTTGTGATGCCGTGCAT	120		
DB	61	CTTCTCTCAGGCTCTCATCTGTGCAACTGTGTGTGTCACTGTGTCTTGTGATGCCGTGCAT	120		
QY	121	CCCCAGAGGTGGCCCCGGATCAGAGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGAAA	180		
DB	121	CCCCAGAGGTGGCCCCGGATGCAAGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGAAA	180		
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DB	241	CCACCCCGAGAGAGAGATCTACCTGTGAGAGAGATCTACCTGTGAGAGAGATCTACT	300		
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DB	361	GAGGCTCTCTGAGATCTCTCAAGAAACCCCAAGTAATATGCCACAGGACAAAGAGGGGAT	420		
QY	421	GACCAAGATCATTTGGCGTATGTAGAGGCGACCGCGCTGTGGCCCGGGGTGTCCCAAGCTTGC	480		
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QY	481	GCGGGCGGCTTCCAGTCCCGGCTGATATCCGCGCCAGAGCTGTGGCCCGGCC	540		
DB	481	GCGGGCGGCTTCCAGTCCCGGCTGATATCCGCGCCAGAGCTGTGGCCCGGCC	540		
QY	541	CTGTGGCCCTCTGGAATCTCTGTGGGCTTCCAGCTCCCGCGCTCCAGAACTGTGGCTGTGC	600		
DB	541	CTGTGGCCCTCTGGAATCTCTGTGGGCTTCCAGCTCCCGCGCTCCAGAACTGTGGCTGTGC	600		
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DB	721	TGCGAGACCACTGTGTGAAGAGCCACCTGTTCCCTGTCCGAGATTCACATGTGTTCACCTCAAG	780		

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DEFINITION Sequence 1 from patent US 5989838.
ACCESSION AR088064
VERSION AR088064.1 GI:10014827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 1 23-NOV-1993;
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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGCAGCCGATGGCTCCCTGTGGCCAGCCCTGAGTCCCTCTGTGATGCCGGCC 60
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DEFINITION ARI04223
ACCESSION ARI04223
VERSION ARI04223.1 GI:12816931
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 1 25-JUL-2000;
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTAGCGGATGCTCCCTGTGCGCCAGCCCGCTGCTCGTTGATCCGAGCC 60
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DEFINITION Sequence 1 from patent US 6204370.
ACCESSION ARI43487
VERSION ARI43487.1 GI:15104773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 1 20-MAR-2001;
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR171392 Sequence 1 from patent US 6297041.
DEFINITION AR171392
ACCESSION AR171392.1 GI:17910342
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 1 02-OCT-2001;
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCC 60
DB 1 ACAGTCAGCCGATGAGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCTCACTGTGCACTGCTGTGCACTGCTGTTCTGATGCTGTCAT 120
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DB 121 CCCGAGAGGTTCCCGGATGAGAGATTTCCCTTGGAGAGGCTTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGAGAGATCTGCCAGTGAAGAGATTTACCCAGAGAGAGAT 240
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QY 301 GAAGTTAAGCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTTT 360
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DB 601 AACCAATGGCCACAGTGTGCACTGACCTGCTCTGGGCTGAGATGCTCTGGGCTGCC 660
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DB 661 GGGCGGAGATACCGGCTCTGCACTGTGCACTGGGGGCTTCAAGTCTCTCGGCG 720

QY 721 TCGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTGGTTCACTCAGC 780
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DB 781 ACCGCTTTTCCAGAGTTGACGAGGCTTTGGGCGCCCGGAGAGGCTTGGCCGTGGCC 840
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LOCUS AR171563 Sequence 1 from patent US 6297051.
DEFINITION AR171563
ACCESSION AR171563
VERSION AR171563.1 GI:17910513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
Zavada, J., Pastorekova, S. and Pastorek, J.
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Location/Qualifiers


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Best Local Similarity	100.0%;	Pred. No. 1.6e-310;		
Matches 1522; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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QY	61 CCGTCTCAAGCCCTCACTGTGCACTGTCACTGTCACTGTCTTGATGCTGTCCAT	120
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QY	121 CCCCAAGAGTTGCCCCGGATGCGAGAGGATTTCCCCCTTGGAGAGAGGCTCTTCTGGGAAA	180
Db	121 CCCCAAGAGTTGCCCCGGATGCGAGAGGATTTCCCCCTTGGAGAGAGGCTCTTCTGGGAAA	180
QY	181 GATGACCCACTGGGCGAGAGGATCTGCCCACTGSAAGAGATTCAACCCAGAGAGAGGAT	240
Db	181 GATGACCCACTGGGCGAGAGGATCTGCCCACTGSAAGAGATTCAACCCAGAGAGAGGAT	240
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QY	361 GAGGCTCTGGAGATCTCTAGAGACCCCAAGATTAATGCCCCAGGGACAAGAGAGGAGAT	420
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QY	481 GCGGCGCGCTTCCAGATCTCCAGAGACCCCAAGATTAATGCCCCAGGGACAAGAGAGGAGAT	540
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QY	661 GGGCGGGAAGTACCGGGCTTTCAGGCTGCACTGTGCACTGTGGGGGCTGCAAGTCTGTCCGGGC	720
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Db	901 GAAAGAAATGCGCTGAGAGAGGCTCAGAGACTCAGGCTCCAGAGACTGAGACATATCTGCACTC	960

Qy	961	CTGCCTCTGACTTCACCCGGTACTTCCAATATAGAGGGTCTCGACTACACCGCCGT	1022
Db	961	CTGCCTCTGACTTCACCCGGTACTTCCAATATAGAGGGTCTCGACTACACCGCCGT	1022
Qy	1021	GCCCAAGGTGTCATCTGSACTGTGTTTAA	1080
Db	1021	GCCCAAGGTGTCATCTGSACTGTGTTTAA	1080
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Db	1081	CACACCTCTCTGACACCTGTGGGGACCTGTGTACCTCTGGCTACAGCTTGAATTCCGA	1144
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FEATURES	Source
LOCUS	BD243152
DEFINITION	NM gene and protein.
ACCESSION	BD243152
VERSION	BD243152.1 GI:33052922
KEYWORDS	JP 2002528085-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 1522)
AUTHORS	Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE	NM gene and protein
JOURNAL	Patent: JP 2002528085-A 1 03-SEP-2002;
COMMENT	INSTITUTE OF VIROLOGY
OS	Homo sapiens (human)
PN	JP 2002528085-A/1
PD	03-SEP-2002
PF	22-OCT-1999 JP 2000578465
PR	23-OCT-1998 US 09/117776 23-OCT-1998 US 09/178115 PT
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C12N15/09, A61K39/395, A61K48/00, A61P35/00, PC	
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CC NM gene and protein	
CC Key	Location/Qualifiers
PH Key	(13) .. (1389)
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FT mat_peptide	Location/Qualifiers
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 71 from Patent EP1439393.
ACCESSION CQ834035
VERSION CQ834035.1 GI:50833640
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Aistle, J.H., Boardman, L.A., Bugarc, L.J., Burgess, C.C., Catino, T.J.,
Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.B., Maimonis, P.J.,
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and
Molino, G.A. Detection methods using T1MP 1 for colon cancer diagnosis
Patent: EP 1439393-A 71 21-JUL-2004;
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
AND RESEARCH (US)
FEATURES
source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX332607 1552 bp DNA linear PAT 09-JUN-2002
DEFINITION Sequence 3116 from Patent WO0194629.
ACCESSION AX332607
VERSION AX332607.1 GI:18123241
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1
Young, P.B., Augustus, M., Carter, K.C., Ehner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 1.6e-310; Indels 0; Gaps 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 151 CCCAGAGAGTTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210
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Qy 301 GAAAGTTAAGCTTAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 331 GAAAGTTAAGCTTAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
Qy 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATATATGCCACAGGAGCAAGAGAGAGAT 420

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Qy	481	GCGGGCCGCTTCCAGTCCCGGGTGAATATCCGCCCCCAAGCTGCAGCTTCGACCAGC	540
Db	511	GCGGGCCGCTTCCAGTCCCGGGTGAATATCCGCCCCCAAGCTGCAGCTTCGACCAGC	570
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Qy	901	GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGATCCAGAGCTGAGACATATCTGCACTC	960
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		VERSION	AX333244.1				
		KEYWORDS	GI:18123878				
		SOURCE					
		ORGANISM	Homo sapiens (human)				
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		REFERENCE					
		AUTHORS	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,				
		TITLE	Horrigan, S., Soppet, D.R. and Weaver, Z.				
			Cancer gene determination and therapeutic screening using signature				
		JOURNAL	Patent: WO 0194629-A 3753 13-DEC-2001;				
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		Best Local Similarity	100.0%; Pred. No. 1,6e-310;				
		Matches 1522; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Qy	Db	91	CTGCTCCAGGCGCTCACTGTGCAACCTGCTGTCATCTGCTGCTTCTGATCGTCCAT	150			
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Qy	Db	361	GAGGCTCTTGAGATCTCTCAAGAACCCCAAGTAAATGCCCCAAGAGCAAGAGAGGAT	420			
Qy	Db	391	GAGGCTCTTGAGATCTCTCAAGAACCCCAAGTAAATGCCCCAAGAGCAAGAGAGGAT	450			
Qy	Db	421	GACCAAGATCATTTGGAGCTATGAGAGGAGACCCGCGCTTGACCCGGAGTCCCCAGCTGC	480			
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Qy	Db	541	CTGGCGCGCTTCCAGTCCCGGTGATATCCGCCAGCTGCGCGCTTTCGCGCGGC	600			

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Db 931 GAAAGAAATGCTGAGAGAGGCTTCAAGTCAAGTCCAGACTGAGACATATCTGACTC 990
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LOCUS AX336174 1552 bp DNA linear PAT 09-JUN-2002
DEFINITION Sequence 6683 from Patent WO0194629.
ACCESSION AX336174
VERSION AX336174.1 GI:18126893

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1,66-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KEYWORDS transmembrane glycoprotein.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1552)
AUTHORS Pastorek J.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1992) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Bratislava 9, 842 46 Bratislava, SLOVAK
REPUBLIC
REMARK revised by [3] MAT

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REFERENCE 2 (bases 1 to 1552)
AUTHORS Pastorek J., Pastorekova S., Callebaut I., Mornon J., Zelink V.,
Opavsky R., Zatovalova M., Liao S., Portetlelle D., Stanbidge E.J.,
Zavada J. and Burny A.
TITLE Cloning and characterization of MN, a human tumor-associated
protein with a domain homologous to carbonic anhydrase and a
putative helix-loop-helix DNA binding segment
JOURNAL Oncogene 9 (10), 2877-2888 (1994)
MEDLINE 9436734
PUBMED 8084592
REFERENCE 3 (bases 1 to 1552)
AUTHORS Pastorek J.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1994) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Bratislava 9, 842 46 Bratislava, SLOVAK
REPUBLIC
REMARK revised by [4] MAT
REFERENCE 4 (bases 1 to 1552)
AUTHORS Pastorek J.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Bratislava 9, 842 46 Bratislava, SLOVAK
REPUBLIC
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ORIGIN

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Query Match 100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
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QY 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 271 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
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QY 901 GAAAGAAATCGCTGAGAGAGGCTCAAGAGATCAAGTCTCCAGGACTGAGACATCTGCACTC 960
DB 931 GAAAGAAATCGCTGAGAGAGGCTCAAGAGATCAAGTCTCCAGGACTGAGACATCTGCACTC 990
QY 961 CTGCGCTCTGACTTCAAGCGGCTACTTCAATTAAGAGGCTCTCTGACTCAACCGCGCTGT 1020
DB 991 CTGCGCTCTGACTTCAAGCGGCTACTTCAATTAAGAGGCTCTCTGACTCAACCGCGCTGT 1050
QY 1021 GCCCAAGGCTGATCTGACTGTGTGTTAAACAGACAGTATGCTGAGTCTAAGCACTC 1080
DB 1051 GCCCAAGGCTGATCTGACTGTGTGTTAAACAGACAGTATGCTGAGTCTAAGCACTC 1110
QY 1081 CACACCTCTGACTTCAAGCGGCTGAGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
DB 1111 CACACCTCTGACTTCAAGCGGCTGAGGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1170
QY 1141 GCGAGCGACCTTGTGAAATGAGGAGTGAAGGCTCTCTCTGCTGAGTGAAGCAAGC 1200
DB 1171 GCGAGCGACCTTGTGAAATGAGGAGTGAAGGCTCTCTCTGCTGAGTGAAGCAAGC 1230
QY 1201 AGTCTCTGGGCTGCTGAGCGAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1231 AGTCTCTGGGCTGCTGAGCGAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1290
QY 1261 GCCCTGTGTTTGGCGCTCTTGTGTGTCACCAAGGTGCGGTCTTGTGCAATGAGA 1320

DB 1291 GCGCGGTTTGTGCGCTCTTTTGTCTGTCAACAGCGTCCGGTCTCTGTGCAAGTGAAGA 1350
QY 1321 AGGCAAGCACAAGAGGAGAACCAAGAGGAGTGTGAGCTACCGCCAGAGAGAGTACCGAG 1380
DB 1351 AGGCAAGCACAAGAGGAGAACCAAGAGGAGTGTGAGCTACCGCCAGAGAGAGTACCGAG 1410
QY 1381 ACTGAGGCTGAGAGGAGTGTGAGAGATGTGAGAGAGAGAGAGAGAGAGATCTGAGAGG 1440
DB 1411 ACTGAGGCTGAGAGGAGTGTGAGAGATGTGAGAGAGAGAGAGAGAGAGATCTGAGAGG 1470
QY 1441 GAGGCGGTAACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500
DB 1471 GAGGCGGTAACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1530
QY 1501 TTTTAAATTAATTAATTTTAAAT 1522
DB 1531 TTTTAAATTAATTAATTTTAAAT 1552

Search completed: February 6, 2005, 05:55:03
Job time : 6361 secs

XX MN gene, protein and nucleic acid fragments - used as primers and probes
PT in the detection of MN antigens and antibodies, and in the treatment of
PT (pre)neoplastic disease.

XX Claim 1, Fig 1, 102pp; English.

XX The present sequence is the full length MuTu endogenous cellular
CC component, MN, cDNA clone, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected Hela cells. Persistent LCMV, the
CC exogenous MuTu transmissible agent (MX), infection increases the
CC expression level of the MN gene. MN is a putative oncogene, and can
CC therefore be used in the development of prods. for the diagnosis and
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC vaccine contg. immunogenic amounts of the MN protein can be used to
CC immunise a vertebrate against a NP disease associated with MN antigen
CC expression. (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 2; Length 1522;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGCGATGAGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGACC 60
DB 1 ACAGTCAGCGCGATGAGCTCCCTGTCGCCAGCCCTGAGCTCCCTGTTGATCCCGACC 60
QY 61 CCGTCGCCAGGCTCCTGTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CCGTCGCCAGGCTCCTGTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCCGAGAGGTTGCCCGGATGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAGA 180
DB 121 CCCGAGAGGTTGCCCGGATGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAGA 180
QY 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
QY 241 CCAACCCGAGAGAGAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT 300
DB 241 CCAACCCGAGAGAGAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT 300
QY 301 GAAGTTAAGCTTAATCAGAGAAGAGAGCTCCCTGAAGTTAAGAGATCTACCTGTT 360
DB 301 GAAGTTAAGCTTAATCAGAGAAGAGAGCTCCCTGAAGTTAAGAGATCTACCTGTT 360
QY 361 GAGGCTCTGAGAGATCTTAAGAACCCAGAAATATGCCACAGGACAAAGAGAGAT 420
DB 361 GAGGCTCTGAGAGATCTTAAGAACCCAGAAATATGCCACAGGACAAAGAGAGAT 420
QY 421 GACGAGATCATTTGGGCTATGAGAGCGACCCGCTGAGCCCGGAGTGCCTCCAGCTGC 480
DB 421 GACGAGATCATTTGGGCTATGAGAGCGACCCGCTGAGCCCGGAGTGCCTCCAGCTGC 480
QY 481 GCGGGGCGGCTTCAAGTCCCGGATGATCCGCCCCAGCTGAGCTTCTGCGCGACC 540
DB 481 GCGGGGCGGCTTCAAGTCCCGGATGATCCGCCCCAGCTGAGCTTCTGCGCGACC 540
QY 541 CTGCGGCTCTGAGAACTCTGAGCTTCCAGCTCCGCGCTCCAGAACTGGCGCTGGGC 600
DB 541 CTGCGGCTCTGAGAACTCTGAGCTTCCAGCTCCGCGCTCCAGAACTGGCGCTGGGC 600
QY 601 AACCAATGCGCAGATGTGCAACTGACCTGCTCTGAGCTGAGATGGCTCTGGAGTCCC 660
DB 601 AACCAATGCGCAGATGTGCAACTGACCTGCTCTGAGCTGAGATGGCTCTGGAGTCCC 660
QY 661 GGGCGGAGATACCGGGCTCTGCAAGCTGATCTGCACTGGGGGGCTGCAAGTGTCTCGGGC 720
DB 661 GGGCGGAGATACCGGGCTCTGCAAGCTGATCTGCACTGGGGGGCTGCAAGTGTCTCGGGC 720

QY 721 TCGAGCACTGTGGAAGGCCACCGCTTCCCTGCGAGATCCAGTGTTCACCTCAGC 780
DB 721 TCGAGCACTGTGGAAGGCCACCGCTTCCCTGCGAGATCCAGTGTTCACCTCAGC 780
QY 781 ACCGCTTTGCAAGATTTGAGAGGCTTTGGGGGCGCCGGAGAGGCTGGCGTGTGGCC 840
DB 781 ACCGCTTTGCAAGATTTGAGAGGCTTTGGGGGCGCCGGAGAGGCTGGCGTGTGGCC 840
QY 841 GCTTTCTGAGAGAGGCGCCGAGAAAGAAAGATGCTATGAGAGATTTGCTGCTGCTTG 900
DB 841 GCTTTCTGAGAGAGGCGCCGAGAAAGAAAGATGCTATGAGAGATTTGCTGCTGCTTG 900
QY 901 GAAGAATGCTGAGAGAGGCTCAGAGACTGAGATCCAGAGATGAGATATCTGCACTC 960
DB 901 GAAGAATGCTGAGAGAGGCTCAGAGACTGAGATCCAGAGATGAGATATCTGCACTC 960
QY 961 CTGCGCTGCACTTCAAGCGCTACTTCCAAATATGAGGGGTCTGATCAACCGCCCTGT 1020
DB 961 CTGCGCTGCACTTCAAGCGCTACTTCCAAATATGAGGGGTCTGATCAACCGCCCTGT 1020
QY 1021 GCCGAGGCTGATCTGAGCTGTGTTTAAACGACAGATGATGATGCTTAAGCAGCTC 1080
DB 1021 GCCGAGGCTGATCTGAGCTGTGTTTAAACGACAGATGATGATGCTTAAGCAGCTC 1080
QY 1081 CACACCTCTCTGACACCTCTGTGGAGACTGTGTGCTCTGCGCTTACAGCTGAACTTCCGA 1140
DB 1081 CACACCTCTCTGACACCTCTGTGGAGACTGTGTGCTCTGCGCTTACAGCTGAACTTCCGA 1140
QY 1141 GCGAGCGAGCTTTGAATGGGCGAGATGATGAGGCTCTCCCTGCTGAGTGGAGCAGC 1200
DB 1141 GCGAGCGAGCTTTGAATGGGCGAGATGATGAGGCTCTCCCTGCTGAGTGGAGCAGC 1200
QY 1201 AGTCTCGGAGCTGTGAGCCAGTCAAGTGAATCTGCTGAGCTGTGAGATCTCTA 1260
DB 1201 AGTCTCGGAGCTGTGAGCCAGTCAAGTGAATCTGCTGAGCTGTGAGATCTCTA 1260
QY 1261 GCGCTGCTTTTGGCTCTCTTTTGGCTGTCAACAGCGCTGGGCTCTTGTGCAAGTGA 1320
DB 1261 GCGCTGCTTTTGGCTCTCTTTTGGCTGTCAACAGCGCTGGGCTCTTGTGCAAGTGA 1320
QY 1321 AGGCGACAGAGAAGGAGAAACAAAGGGGCTGTGAGTACCGCCAGCAGAGAGTACCGAG 1380
DB 1321 AGGCGACAGAGAAGGAGAAACAAAGGGGCTGTGAGTACCGCCAGCAGAGAGTACCGAG 1380
QY 1381 ACTGAGCTTGAAGAGCTGAGATCTTGAAGATGTGAGAGCCAGCAGAGGATCTGAGGG 1440
DB 1381 ACTGAGCTTGAAGAGCTGAGATCTTGAAGATGTGAGAGCCAGCAGAGGATCTGAGGG 1440
QY 1441 GAGCCGGTAACTGTCTCTGCTCTCAATATGCACTTCTTTTAACTGCAAGAAAT 1500
DB 1441 GAGCCGGTAACTGTCTCTGCTCTCAATATGCACTTCTTTTAACTGCAAGAAAT 1500
QY 1501 TTTTAAATATAATTTTAAAT 1522
DB 1501 TTTTAAATATAATTTTAAAT 1522
RESULT 2
AA1540
ID AA1540 standard; cDNA; 1522 BP.
XX
AC AAA1540;
XX
DT 16-JUN-2000 (first entry)
XX
DE Human MN protein encoding cDNA seq ID NO:1.
XX
KM Human, MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KM oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KM MN/CA IX isoenzyme; ds.
XX
OS Homo sapiens.

XX US6027887-A.
PN
XX
PD 22-FEB-2000.
XX
PF 24-JAN-1997; 97US-00787739.
XX
PR 21-OCT-1992; 92US-00964589.
PR 30-DEC-1993; 93US-00177093.
PR 15-JUN-1994; 94US-00260190.
PR 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
XX 07-JUN-1995; 95US-00487077.
XX
XX (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
PI Pastorek J, Zavada J, Pastorekova S;
XX WPI; 2000-194827/17.
DR P-PSDB; AAY53228.
XX
XX Nucleic acid based assay for diagnosing a wide variety of
PT preneoplastic/neoplastic disease comprises screening for the presence of
PT abnormal MN gene expression in a vertebrate.
XX
XX Claim 1; Fig 1; 87p; English.
XX
XX The present invention describes a method of screening for
CC preneoplastic/neoplastic disease. The method comprises: (1) determining
CC whether abnormal MN gene expression is present in a vertebrate; and (2)
CC if abnormal MN gene expression is determined to be present in the
CC vertebrate, determining that the vertebrate has a significant risk of
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC in a vertebrate, preferably a human. The disease detected is mammary,
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC mucosa, pancreatic duct epithelium or liver duct epithelium
CC preneoplastic/neoplastic disease. AAY16540 to AAY16617 and AAY53228 to
CC AAY53245 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGCTCCCTGTGCCCCAGGCCCTGCTCCCTGTGATCCCGGCC 60
DB 1 ACAGTCAGCCGATGCTCCCTGTGCCCCAGGCCCTGCTCCCTGTGATCCCGGCC 60
QY 61 CCTGTCCAGGCTCTCATCTGTGCACTGCTGCTGTCACTGCTGTTTGATGCTGTCCAT 120
DB 61 CCTGTCCAGGCTCTCATCTGTGCACTGCTGCTGTCACTGCTGTTTGATGCTGTCCAT 120
QY 121 CCCCAAGAGTTGCCCGGATGAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGAAA 180
DB 121 CCCCAAGAGTTGCCCGGATGAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGAAA 180
QY 181 GATGACCCACTGAGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 181 GATGACCCACTGAGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240

QY 241 CCACCCGAGAGAGAGATCTACCTTGAGAGAGATCTACCTTGAGAGAGATCTACCT 300
DB 241 CCACCCGAGAGAGAGATCTACCTTGAGAGAGATCTACCTTGAGAGAGATCTACCT 300
QY 301 GAAATTAACTTAATCAGAAAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGTT 360
DB 301 GAAATTAACTTAATCAGAAAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGTT 360
QY 361 GAGGCTCCCTGAGATCTCTCAAGAACCCCGAGATTAAAGCCCAAGAGAAAGAGGAT 420
DB 361 GAGGCTCCCTGAGATCTCTCAAGAACCCCGAGATTAAAGCCCAAGAGAAAGAGGAT 420
QY 421 GACCAAGATCATTTGGGCTATGAGAGGCGAGCCGCTGAGCCCGGGGTGCCAGGCTCC 480
DB 421 GACCAAGATCATTTGGGCTATGAGAGGCGAGCCGCTGAGCCCGGGGTGCCAGGCTCC 480
QY 481 GCGGGCCGCTTCAAGTCCCGGTGATATCCGCCCAAGCTGAGCTTCTGCCCCGAGC 540
DB 481 GCGGGCCGCTTCAAGTCCCGGTGATATCCGCCCAAGCTGAGCTTCTGCCCCGAGC 540
QY 541 CTGCGCCCTTGAAACTCTGAGCTTCCAGCTCCGCGCTCCAGAACTGCGCTCGCC 600
DB 541 CTGCGCCCTTGAAACTCTGAGCTTCCAGCTCCGCGCTCCAGAACTGCGCTCGCC 600
QY 601 AACAAATGACCAAGTGTGCACTGACCCCTGCTGAGGCTGAGATGAGCTGAGGTCCTC 660
DB 601 AACAAATGACCAAGTGTGCACTGACCCCTGCTGAGGCTGAGATGAGCTGAGGTCCTC 660
QY 661 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGAGGAGGCTGCAAGTGTCCGGGC 720
DB 661 GGGCGGAGTACCGGCTCTGAGCTGATCTGCACTGAGGAGGCTGCAAGTGTCCGGGC 720
QY 721 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCGAGATCAAGTGTCTCACTCAGC 780
DB 721 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCGAGATCAAGTGTCTCACTCAGC 780
QY 781 ACCGCTTTCAGAGTTGACAGAGGCTTGGGGCGCCGGAGGCTGCGCTGCTGGCC 840
DB 781 ACCGCTTTCAGAGTTGACAGAGGCTTGGGGCGCCGGAGGCTGCGCTGCTGGCC 840
QY 841 GCTTTCTGAGAGAGGCGCCGAGAGAAAACAGTGTCTATGACAGTGTCTGCTGCTGG 900
DB 841 GCTTTCTGAGAGAGGCGCCGAGAGAAAACAGTGTCTATGACAGTGTCTGCTGCTGG 900
QY 901 GAAAGAAATGCTGAGAGAGGCTCAAGACTCAGGCTCCAGAGACTGAGATATCTGCACTC 960
DB 901 GAAAGAAATGCTGAGAGAGGCTCAAGACTCAGGCTCCAGAGACTGAGATATCTGCACTC 960
QY 961 CTGCCCTGATCAGCCGCTAATTCATATGAGGGGTCTGTGACTACACCGCCCTGT 1020
DB 961 CTGCCCTGATCAGCCGCTAATTCATATGAGGGGTCTGTGACTACACCGCCCTGT 1020
QY 1021 GCCCAGGGTGTATCTGACTGTGTTAAACAGACAGTATCTGAGTCTAAGCAGCTC 1080
DB 1021 GCCCAGGGTGTATCTGACTGTGTTAAACAGACAGTATCTGAGTCTAAGCAGCTC 1080
QY 1081 CACACCTTCTGACACCTCTGTGAGGAGCTGTGTAATCTGAGCTACAGTGAATCTTCGA 1140
DB 1081 CACACCTTCTGACACCTCTGTGAGGAGCTGTGTAATCTGAGCTACAGTGAATCTTCGA 1140
QY 1141 GCGAGCGAGCTTTAAATGAGGAGATGATGAGGCTCTTCCCTGCTGAGATGAGACAGC 1200
DB 1141 GCGAGCGAGCTTTAAATGAGGAGATGATGAGGCTCTTCCCTGCTGAGATGAGACAGC 1200
QY 1201 AGTCTCGGGCTGTGAGCAGTCAAGCTGAATCTCTGCTGAGCTGAGTGAATCTCTA 1260
DB 1201 AGTCTCGGGCTGTGAGCAGTCAAGCTGAATCTCTGCTGAGCTGAGTGAATCTCTA 1260
QY 1261 GCTCTGTTTGTGCTCTCTTCTGCTGACACAGCTGCGCTTCTTGTGCAATGAGA 1320
DB 1261 GCTCTGTTTGTGCTCTCTTCTGCTGACACAGCTGCGCTTCTTGTGCAATGAGA 1320
QY 1321 AGGCAAGCACAAAGGGAAACAAAGGGGTGTGACTACCGCCAGAGAGATACCCAG 1380

Dd		1321	AGGACGACACAGAAGGGGAACCAAGAGGGGTGTGACTTACCCTCCAGCAGAGAGGTACCGAG	1380
Oy		1381	ACTGGAGCCTTAGAGCCTGGATCTTGAGAAATGTGAAAGCCAGGCCAAGGCATCTGAGGG	1440
Dd		1381	ACTGAGCCTTAGAGCCTGGATCTTGAGAAATGTGAAAGCCAGGCCAAGGCATCTGAGGG	1440
Oy		1441	GGAAGCGGTAACTGCTGTCCTGCTCATTTATGACCTCTTTAACTGCAACAATAAT	1500
Dd		1441	GGAAGCGGTAACTGCTGCTGCTCATTTATGACCTCTTTAACTGCAACAATAAT	1500
Oy		1501	TTTTTAATAATAATTATTAAT	1522
Dd		1501	TTTTTAATAATAATTATTAAT	1522
 RESULT 3 AAA52459 standard; cDNA, 1522 BP.				
XX	AAAS2459;			
XX	25-SEP-2000	(first entry)		
De	Human MN CDNA.			
KX	MN protein; tumour associated cell adhesion molecule; oncoprotein;			
KV	proteoglycan domain; PG domain; carbonic anhydrase; Ca domain;			
KM	abnormal expression; neoplastic disease; cancer; gene therapy; ss.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	CDS	13..1392		
FT		/tag= a		
XX		/product= "Human MN protein"		
Pn	WO200024913-A2.			
Pd	04-MAY-2000.			
Pf	22-OCT-1999;	99WO-US024879.		
Pr	23-OCT-1998;	98US-00177776.		
Xx	23-OCT-1998;	98US-00178115.		
Pa	(FARB) BAYER CORP.			
Pi	(VIRO-) INST VIROLOGY.			
Dr	Zavada J., Pastorekova S, Pastorek J;			
Dx	WPI; 2000-350752/30.			
DR	P-PSDB; AAB03005.			
 A molecule which specifically binds to a site on MN protein (oncoprotein) and prevents adhesion of vertebrate cells to the protein, useful for treating preneoplastic or neoplastic diseases such as cancer.				
 Example 1; Fig 1A-C; 154pp; English.				
CC	The invention relates to the inhibition of cell adhesion mediated by the			
CC	MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250			
CC	protein). The MN protein is a tumour-associated adhesion molecule which			
CC	comprises a proteoglycan-like (PG) domain (AAB03017) which contains the			
CC	protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).			
CC	Abnormal expression of the MN protein is associated with tumorigenicity.			
CC	The invention encompasses molecules (e.g., proteins and peptides) which			
CC	which specifically bind to a site on the MN protein, thereby preventing			
CC	adhesion of vertebrate cells to the protein in a cell adhesion assay. It			
CC	also encompasses MN proteins or MN protein fragments which can be added			
CC	to the extracellular environment to prevent the adhesion of vertebrate			
CC	cells to each other. The invention also relates to the identification of			
CC	the binding site of the MN protein and to a method of identifying a site			

	Query Match	Best Local Similarity	100.0%;	Score 1522;	DB 3;	Length 1522;	
	Matches 1522;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	ACAGTCAAGCGCATGCTCCCTCTGTGCCACAGCCCTTGCTCCTCTGTGATCCCGGC	60				
Db	1	ACAGTCAAGCGCATGCTCCCTCTGTGCCACAGCCCTTGCTCCTCTGTGATCCCGGC	60				
QY	61	CTGTCTCAAGCCCTCACTGTGCAACTGTGTGCACTGTGTCTTATGCTGTCCAT	120				
Db	61	CTGTCTCAAGCCCTCACTGTGCAACTGTGTGCACTGTGTCTTATGCTGTCCAT	120				
QY	121	CCCGCAGAGTTGCCCCGATGACAGAGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGAA	180				
Db	121	CCCGCAGAGTTGCCCCGATGACAGAGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGAA	180				
QY	121	CCCGCAGAGTTGCCCCGATGACAGAGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGAA	180				
Db	121	CCCGCAGAGTTGCCCCGATGACAGAGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGAA	180				
QY	181	GATGACCCACTGTGGGCGAGAGAGATTCGCCGATGAAGAGATTCACCCAGAGAGAGAT	240				
Db	181	GATGACCCACTGTGGGCGAGAGAGATTCGCCGATGAAGAGATTCACCCAGAGAGAGAT	240				
QY	241	CCACCCGAGAGAGAGATCTACTGTGAGAGAGATCTACTGTGAGAGAGATTTACT	300				
Db	241	CCACCCGAGAGAGAGATCTACTGTGAGAGAGATCTACTGTGAGAGAGATTTACT	300				
QY	301	GAACTTAAGCTTAATCAAGAAAGAGGCTCCTGAAATTAGAGATCTACTGT	360				
Db	301	GAACTTAAGCTTAATCAAGAAAGAGGCTCCTGAAATTAGAGATCTACTGT	360				
QY	361	GAGGCTCTGTGAGATCTCAAGAAACCCAGAAATATGCCCAAGAGAGAGAT	420				
Db	361	GAGGCTCTGTGAGATCTCAAGAAACCCAGAAATATGCCCAAGAGAGAGAT	420				
QY	421	GACCAAGTCAATTGGCGCTATGAGGCGACCCGCTTGAGCCCGGAGTCTCCAGCTGC	480				
Db	421	GACCAAGTCAATTGGCGCTATGAGGCGACCCGCTTGAGCCCGGAGTCTCCAGCTGC	480				
QY	481	GCGGCGCGCTTCCAGTCCCGGAGATATCCGCGCCAGCTCGCGCTTCTGCGCGGCG	540				
Db	481	GCGGCGCGCTTCCAGTCCCGGAGATATCCGCGCCAGCTCGCGCTTCTGCGCGGCG	540				
QY	541	CTGTGCGCCCTTGAACTCTGTGGCTTCAGTCTCCGCGCTCCAGACTGCGCTGCG	600				
Db	541	CTGTGCGCCCTTGAACTCTGTGGCTTCAGTCTCCGCGCTCCAGACTGCGCTGCG	600				
QY	601	AACAAATGGCCCAAGTGTGCACTGACCTCTGCTCTGTGGCTTAAAGATGTGCTGGTCC	660				
Db	601	AACAAATGGCCCAAGTGTGCACTGACCTCTGCTCTGTGGCTTAAAGATGTGCTGGTCC	660				
QY	661	GCGGCGAGTACCGGCGCTCTGAGCTCATCTGACCTGCGGCGCTGACAGTCTGCGGCG	720				
Db	661	GCGGCGAGTACCGGCGCTCTGAGCTCATCTGACCTGCGGCGCTGACAGTCTGCGGCG	720				
QY	721	TCGAGACCACTGTGAGGCGACCGTTTCCCTGCGAGATCACTGTGTTCACTCAAC	780				

DB 721 TGGAGCACACTGTGGAAGGCCACGTTTCCCTGCGGAGATCCAGTGGTTCACTCCAGC 780
QY 781 ACCGCTTTTCCAGAGTTGACAGAGCCTTGGGGGCCCCGAGAGGCTCGCCGTGTGGCC 840
DB 781 ACCGCTTTTCCAGAGTTGACAGAGCCTTGGGGGCCCCGAGAGGCTCGCCGTGTGGCC 840
QY 841 GCGCTTCTGAGAGAGGGCCCGAGAGAAACAGTGCCTATGAGCAGTGTGCTGCTGGCTTG 900
DB 841 GCGCTTCTGAGAGAGGGCCCGAGAGAAACAGTGCCTATGAGCAGTGTGCTGCTGGCTTG 900
QY 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGATCGACATATCTGACATC 960
DB 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGATCGACATATCTGACATC 960
QY 961 CTGCGCTTCTGACTTCAAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGT 1020
DB 961 CTGCGCTTCTGACTTCAAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGT 1020
QY 1021 GCGCAGAGGTGATCTGAGACTGTGTTAACAGACAGTATGCTGAGTGTAGAGACTC 1080
DB 1021 GCGCAGAGGTGATCTGAGACTGTGTTAACAGACAGTATGCTGAGTGTAGAGACTC 1080
QY 1081 CACACCTCTCTGACACACCTGTGGGACCTGTGACTCTCGGCTACAGCTGAATCTCCGA 1140
DB 1081 CACACCTCTCTGACACACCTGTGGGACCTGTGACTCTCGGCTACAGCTGAATCTCCGA 1140
QY 1141 GCGACGACGCTTTGAAATGGGCGAGTGAATGAGGCTCTCTGCTGTGAGTGAACAGC 1200
DB 1141 GCGACGACGCTTTGAAATGGGCGAGTGAATGAGGCTCTCTGCTGTGAGTGAACAGC 1200
QY 1201 AGTCCCTGGGCTGTGAGCAGTGCAGTGAATTCCTGCTGTGCTGTGATCTGATCTGA 1260
DB 1201 AGTCCCTGGGCTGTGAGCAGTGCAGTGAATTCCTGCTGTGCTGTGATCTGATCTGA 1260
QY 1261 GCGCTGTGTTTGGCTCTCTTGTGCTGACACAGGCTGCGCTTCTGCTGTGATGAGA 1320
DB 1261 GCGCTGTGTTTGGCTCTCTTGTGCTGACACAGGCTGCGCTTCTGCTGTGATGAGA 1320
QY 1321 AGGACGACAGAAAGGGGAAACAAAGGGGGGTGTGAGTACCGCCACAGAGTGAAGCCGAG 1380
DB 1321 AGGACGACAGAAAGGGGAAACAAAGGGGGGTGTGAGTACCGCCACAGAGTGAAGCCGAG 1380
QY 1381 ACTGAGGCTTGAAGGCTGTGATCTTGAAGATGTGAAGACGACCCAGAGCATCTGAGG 1440
DB 1381 ACTGAGGCTTGAAGGCTGTGATCTTGAAGATGTGAAGACGACCCAGAGCATCTGAGG 1440
QY 1441 GGAGCGGTAAGTCTGCTGCTGCTCAATTATGCACTTCTTTAACTGCCAAAGAAAT 1500
DB 1441 GGAGCGGTAAGTCTGCTGCTGCTCAATTATGCACTTCTTTAACTGCCAAAGAAAT 1500
QY 1501 TTTTAAATTAATATTTATTAAT 1522
DB 1501 TTTTAAATTAATATTTATTAAT 1522

RESULT 4
ADG31413 standard; cDNA; 1522 BP.
ID ADG31413
XX
AC ADG31413,
XX
DT 26-FEB-2004 (first entry)
XX
DE Human MN cDNA SegID 1.
XX
KW human; gene; ss; monoclonal antibody; MN/CA IX; MN; oncogene;
KW carbonic anhydrase 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
KW neoplastic tumour; cytosolic; cancer; tumour therapy;
KW anti-tumour vaccine.
XX
OS Homo sapiens.
XX

PN W02003100029-A2.
XX
PD 04-DEC-2003.
XX
PF 22-FEB-2003; 2003MO-US005136.
XX
PR 23-MAY-2002; 2002US-0383068P.
PR 05-DEC-2002; 2002US-0431499P.
XX
PA (FARB) BAYER CORP.
PA (VIRI) INST VIROLOGY.
PI Pastorek J, Pastorekova S, Zatoricova M, Zavada J, Orlova Gut M;
PI WPI; 2004-035136/03.
DR P-PSDB; ADG31414.
XX
XX
PT New monoclonal antibody generated from MN/CA IX-deficient mice, where the
PT antibody binds specifically to human tumor-associated cell adhesion
PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 1; 156pp; English.
XX
CC This invention relates to a novel monoclonal antibody identified as the
CC MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
CC mice). Specifically, this antibody is directed towards the MN gene, a
CC cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC present invention describes the generation of this monoclonal antibody,
CC and immunoreactive fragments thereof, which are directed against non-
CC immunodominant epitopes on the CA IX extracellular domain. As such, this
CC antibody can be useful diagnostically as a marker for preneoplastic/
CC neoplastic tumours, immunodetection methods and immunotargeting
CC approaches. Accordingly, compositions exhibit cytostatic activity and are
CC useful in the diagnosis, prognosis and treatment of various cancers
CC including breast, bladder or lung cancer, in tumour therapy and in anti-
CC tumour vaccination. This polynucleotide sequence is the human MN cDNA of
CC the invention.
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 12; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCCCTGTGCTCTGTTGATCCCGGCC 60
DB 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCCCTGTGCTCTGTTGATCCCGGCC 60
QY 61 CCGTCTCAGGCGCTCACTGTGCACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CCGTCTCAGGCGCTCACTGTGCACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCCGAGAGTGGCCCGGATGAGAGAGATTCCTCCCTTGGGAGAGGCTCTTGGGGA 180
DB 121 CCCGAGAGTGGCCCGGATGAGAGAGATTCCTCCCTTGGGAGAGGCTCTTGGGGA 180
QY 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGATGAAGAGATTCAACCCAGAGAGAGAT 240
DB 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGATGAAGAGATTCAACCCAGAGAGAGAT 240
QY 241 CCAACCGGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 241 CCAACCGGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
QY 301 GAAGTTAAACCTTAATCAAGAAGAGGCTCCCTGAAGTGAAGATCTACCTACTGTT 360
DB 301 GAAGTTAAACCTTAATCAAGAAGAGGCTCCCTGAAGTGAAGATCTACCTACTGTT 360
QY 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAATGCCACAGGACAAAGAGGAGAT 420

Db	361	GAAGGCTCTGGAGATTCCTCAAGAACCCCAAGATATATGCCACAGGGACCAAGAAAGGGAT	420
Qy	421	GAACAGATGATTTGGCGCTATATGAGAGCGACCCGCGCTTGAGCGCGGATGTCCCAAGCTGC	480
Db	421	GAACAGAGTCAATTTGGCGCTATATGAGAGCGACCCGCGCTTGAGCGCGGATGTCCCAAGCTGC	480
Qy	481	GGGGGGCGGCTTCAGATGCCCGGGATATTCGGCGCCCAAGTGGCGGCTTTCTGGCCGGGC	540
Db	481	GGGGGGCGGCTTCAGATGCCCGGGATATTCGGCGCCCAAGTGGCGGCTTTCTGGCCGGGC	540
Qy	541	CTGGCGCCCCCTGGAACTCCCTGGCTTTCAGACTCCCGCGCTCCCAAACTGCAGCTGC	600
Db	541	CTGGCGCCCCCTGGAACTCCCTGGCTTTCAGACTCCCGCGCTCCCAAACTGCAGCTGC	600
Qy	601	AACAAATGGCCACAGTGTGAACTGAACCCCGGCTCCCTGGGCTTAAGATATGCTCTGGGTCCC	660
Db	601	AACAAATGGCCACAGTGTGAACTGAACCCCGGCTCCCTGGGCTTAAGATATGCTCTGGGTCCC	660
Qy	661	GGGCGGGAGTACCGGGCTCTGAGAGCTGACATCTGCACTGGGGGGCTCAAGTCCGTCGGGC	720
Db	661	GGGCGGGAGTACCGGGCTCTGAGAGCTGACATCTGCACTGGGGGGCTCAAGTCCGTCGGGC	720
Qy	721	TGGAGACACACTGTGAAAGGCCACCGTTTCCTGCGCAATCCAAGTGTTCACCTCAGC	780
Db	721	TGGAGACACACTGTGAAAGGCCACCGTTTCCTGCGCAATCCAAGTGTTCACCTCAGC	780
Qy	781	ACCGGCTTTGGCAGAGTTGACAGAGGCGCTTGGGGGCGCCGGAGAGCGCTGGCGGTTGGCG	840
Db	781	ACCGGCTTTGGCAGAGTTGACAGAGGCGCTTGGGGGCGCCGGAGAGCGCTGGCGGTTGGCG	840
Qy	841	GCGTTTCTGGAGAGAGGCGCCGGAGAGAAACAGTGCCTATAGCAGTTGTCTGTGCGCTTG	900
Db	841	GCGTTTCTGGAGAGAGGCGCCGGAGAGAAACAGTGCCTATAGCAGTTGTCTGTGCGCTTG	900
Qy	901	GAAGAAATCGCTGAGAGAGGCTCAGAGACTCAAGTCCAGAGCTGGAACATATCTGCACATC	960
Db	901	GAAGAAATCGCTGAGAGAGGCTCAGAGACTCAAGTCCAGAGCTGGAACATATCTGCACATC	960
Qy	961	CTGCGCTCTGACCTTCAAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGGCGTGT	1020
Db	961	CTGCGCTCTGACCTTCAAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGGCGTGT	1020
Qy	1021	GCCCAAGGATCATCTGACATCTGTGTTTAAACAAGATATGCTAGTCTTAAGACATCTC	1080
Db	1021	GCCCAAGGATCATCTGACATCTGTGTTTAAACAAGATATGCTAGTCTTAAGACATCTC	1080
Qy	1081	CACACCTCTCTGACACCTGTGGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCCGA	1140
Db	1081	CACACCTCTCTGACACCTGTGTGGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCCGA	1140
Qy	1141	GCGAGCAGGCTTTGAATGGCGAGTGAATGAGGCTCTCTTCCCTGCTGAGATGGAACAGC	1200
Db	1141	GCGAGCAGGCTTTGAATGGCGAGTGAATGAGGCTCTCTTCCCTGCTGAGATGGAACAGC	1200
Qy	1201	AGTCTCGGGGCTGAGAGCACTGATTCAGAGTTCCTGCTGAGGCTGTGGGTGATCAATCTTA	1260
Db	1201	AGTCTCGGGGCTGAGAGCACTGATTCAGAGTTCCTGCTGAGGCTGTGGGTGATCAATCTTA	1260
Qy	1261	GCCCTGATTTTGGGCTCTCTTTTCTGTCAACACAGCTGTGCGTTCTTGTGCAATGAGA	1320
Db	1261	GCCCTGATTTTGGGCTCTCTTTTCTGTCAACACAGCTGTGCGTTCTTGTGCAATGAGA	1320
Qy	1321	AGGCAAGCACAAAGGGGAAACCAAAGGGGTGTGAATTCACCGCCACAGAGATTAACCGAG	1380
Db	1321	AGGCAAGCACAAAGGGGAAACCAAAGGGGTGTGAATTCACCGCCACAGAGATTAACCGAG	1380
Qy	1381	ACTGAGGCTTGAAGGCTGATCTTGTGAGATGTGAAAGCCAGCAGAGGCAATCTGAGGG	1440
Db	1381	ACTGAGGCTTGAAGGCTGATCTTGTGAGATGTGAAAGCCAGCAGAGGCAATCTGAGGG	1440
Qy	1441	GGAGCGGATTAATGTCTGTCTCTGTCTCATATATGCACTTCTTTTAACTGCCAAGAAAT	1500
Db	1441	GGAGCGGATTAATGTCTGTCTCTGTCTCATATATGCACTTCTTTTAACTGCCAAGAAAT	1500

QY	1501	TTTTAAATTAATATTATAT	1522
DB	1501	TTTTAAATTAATATTATAT	1522
RESULT 5			
ADK41803	ID	ADK41803 standard; DNA; 1522 BP.	
XX	ADK41803;		
XX	06-MAY-2004 (first entry)		
DE	Human MN gene sequence Seg1D1.		
KW	carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;		
KW	human; vertebrate; cytostatic; vaccine; gene therapy;		
KW	renal cell carcinoma; breast cancer; colorectal cancer; ds; gene.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	13..1392	
FT	FT	/*tag = a	
FT	FT	/product= "Human MN protein"	
PN	WO2004005348-A1.		
PD	15-JAN-2004.		
PF	22-FEB-2003; 2003WO-US005137.		
PR	23-MAY-2002; 2002US-0383068P.		
PR	05-DEC-2002; 2002US-0431499P.		
XX	(FARB) BAYER CORP.		
PA	(VITRO-) INST VIROLOGY.		
PI	Zavada J, Pastorekova S, Pastorek J, Zavadova Z;		
XX	WPI; 2004-083500/08.		
DR	P-PSDB; ADK41804.		
XX			
PT	New soluble form of the carbonic anhydrase IX (CA IX) protein for		
PT	screening, diagnosing or prognosing diseases associated with abnormal		
PT	expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or		
PT	colorectal cancer.		
XX			
PS	Disclosure; SEQ ID NO 1, 159pp; English.		
XX			
CC	This invention relates to a novel soluble form of the carbonic anhydrase		
CC	IX (CA IX) (or MN) protein or CA IX polypeptide which is released from		
CC	precancerous and/or cancerous cells of a vertebrate into a body fluid.		
CC	The invention may be useful for the development of compounds with a		
CC	cytostatic activity or a vaccine whilst the disclosed sequences may be		
CC	used for gene therapy. The protein and method are useful for screening,		
CC	diagnosing or prognosing diseases associated with abnormal expression of		
CC	carbonic anhydrase IX protein, such as precancerous and cancerous		
CC	diseases like renal cell carcinoma, breast cancer or colorectal cancer.		
CC	The monoclonal antibody may also be used for treating or preventing		
CC	precancerous and cancerous diseases. The present sequence is that of the		
CC	gene which encodes the human MN protein of the invention.		
XX			
XX	Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;		
XX			
QY	Query Match	100.0%; Score 1522; DB 12; Length 1522;	
XX	Best Local Similarity	100.0%; Pred. No. 0;	
XX	Matches 1522; Conservative	0; Mismatches	0; Indels
XX			Gaps
XX			0;
DB	1	ACAGTACGCCGATGCTCCCTGTGTGCCACAGCCCTGTGCTCTGTGTATCCGGCC	60
DB	1	ACAGTACGCCGATGCTCCCTGTGTGCCACAGCCCTGTGCTCTGTGTATCCGGCC	60

PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PR, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX WPI, 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, and determining a change
XX in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 3116; 44dp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
XX neoplastic agent. The method involves exposing cells to a chemical agent
XX to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX to ABL70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening an
XX anti-neoplastic agent, and can be used for producing a product which is
XX the data collected with respect to the anti-neoplastic agent as a result
XX of M1, and the data is sufficient to convey the chemical structure and/or
XX properties of the agent. M1 can be used in the treatment of cancer such
XX as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
XX prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell,
XX cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
XX cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
XX tumour
XX
XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGATGCTCCCTGTGCCAGCCCTGAGCTCCCTGTGTGATCCGAGCC 60
DB 31 ACAGTCAGCCGATGCTCCCTGTGCCAGCCCTGAGCTCCCTGTGTGATCCGAGCC 90
QY 61 CCTGCTCCAGGCTCACTGTGCACTGCTGTGCACTGTGCTTGTATGCTGTCCAT 120
DB 91 CCTGCTCCAGGCTCACTGTGCACTGCTGTGCACTGTGCTTGTATGCTGTCCAT 150
QY 121 CCCGAGGTTGGCCCGATGAGAGATGATCCCTTGGAGAGAGGCTTTTGGGAA 180
DB 151 CCCGAGGTTGGCCCGATGAGAGATGATCCCTTGGAGAGAGGCTTTTGGGAA 210
QY 181 GATGACCACTGGGAGAGAGATGATGCTGCTGAGAGAGATTTCCAGAGAGAGAT 240

DB 211 GATGACCACTGGGAGAGAGATGATGCTGCTGAGAGATTTCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTACTGTGAGAGAGATCTACTGTGAGAGAGATCTACT 300
DB 271 CCACCCGAGAGAGAGATCTACTGTGAGAGAGATCTACTGTGAGAGAGATCTACT 330
QY 301 GAAGTTAAGCTTAATCAAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 390
QY 361 GAGGCTCTGAGAGATCTCAAGAAACCCCAAGATATATGCCACAGAGACAAAGAGGAT 420
DB 391 GAGGCTCTGAGAGATCTCAAGAAACCCCAAGATATATGCCACAGAGACAAAGAGGAT 450
QY 421 GACCAAGTCAATGAGCGCTATGAGAGCGACCCGCTGTGACCCGAGTGTCCAGCTGC 480
DB 451 GACCAAGTCAATGAGCGCTATGAGAGCGACCCGCTGTGACCCGAGTGTCCAGCTGC 510
QY 481 GCGGCGCGCTCCAGATCCCGCGTGATATCCGCGCCCAAGCTGCGCTTCTGCGCGGCC 540
DB 511 GCGGCGCGCTCCAGATCCCGCGTGATATCCGCGCCCAAGCTGCGCTTCTGCGCGGCC 570
QY 541 CTGCGCGCCCTGGAATCTGAGGCTTCAGGCTCCGCGCTCCGAGAACTGCGCTGCGC 600
DB 571 CTGCGCGCCCTGGAATCTGAGGCTTCAGGCTTCGCGCTCCGAGAACTGCGCTGCGC 630
QY 601 AACATGCGCACTGTGCACTGACCTGCTCTGAGCTGAGATGCTGTGAGTCC 660
DB 631 AACATGCGCACTGTGCACTGACCTGCTCTGAGCTGAGATGCTGTGAGTCC 690
QY 661 GGGGGGAGATACCGGCTCTGACAGTCAATGCACTGGGGGCTGCAAGTGTCCGAGC 720
DB 691 GGGGGGAGATACCGGCTCTGACAGTCAATGCACTGGGGGCTGCAAGTGTCCGAGC 750
QY 721 TCGAGCACTGTGAAAGGCAACGTTTCCCTCCAGATCCAGTGTGTTCACTGAC 780
DB 751 TCGAGCACTGTGAAAGGCAACGTTTCCCTCCAGATCCAGTGTGTTCACTGAC 810
QY 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGGCGCCCGAGAGGCTTGGCTTGGCC 840
DB 811 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGGCGCCCGAGAGGCTTGGCTTGGCC 870
QY 841 GCTTTTCTGAGAGAGGCGCGGAGAAACAGTTCATATGAGAGTGTCTCTGCTTG 900
DB 871 GCTTTTCTGAGAGAGGCGCGGAGAAACAGTTCATATGAGAGTGTCTCTGCTTG 930
QY 901 GAAGAAATCGCTGAGAGAGGCTCAGAGCTCAGAGTCCAGAGCTGACATATCTGACTC 960
DB 931 GAAGAAATCGCTGAGAGAGGCTCAGAGCTCAGAGTCCAGAGCTGACATATCTGACTC 990
QY 961 CTGCTCTGATCTTCAAGCCGCTTCAATATGAGAGGCTTCTGACTACAGCGCCCTGT 1020
DB 991 CTGCTCTGATCTTCAAGCCGCTTCAATATGAGAGGCTTCTGACTACAGCGCCCTGT 1050
QY 1021 GCCAGAGGTGATCTGAGAGCTGTGTTTAAACAGACAGAGTGTGAGTGTGTAACAGCTC 1080
DB 1051 GCCAGAGGTGATCTGAGAGCTGTGTTTAAACAGACAGAGTGTGAGTGTGTAACAGCTC 1110
QY 1081 CACACCTCTCTGACACCTGTGAGGACCTGTGATCTCTGAGCTGACAGTGAATCTCCGA 1140
DB 1111 CACACCTCTCTGACACCTGTGAGGACCTGTGATCTCTGAGCTGACAGTGAATCTCCGA 1170
QY 1141 GCGAGCGAGCTTTGAATGAGCGAGATGATGAGGCTCTTCCCTGCTGAGTGAAGC 1200
DB 1171 GCGAGCGAGCTTTGAATGAGCGAGATGATGAGGCTCTTCCCTGCTGAGTGAAGC 1230
QY 1201 AGTCTGAGGCTGTGAGCGAGTCAAGTGAATTCGAGCGAGTGTGAGTGAATCTCTA 1260
DB 1231 AGTCTGAGGCTGTGAGCGAGTCAAGTGAATTCGAGCGAGTGTGAGTGAATCTCTA 1290
QY 1261 GCGCTGAGTTTGTGCTCTTTTGTGCTGACAGAGCTGCGCTTCTTGTGCAATGAGA 1320
DB 1291 GCGCTGAGTTTGTGCTCTTTTGTGCTGACAGAGCTGCGCTTCTTGTGCAATGAGA 1350

QY 1321 AGGACGACAGAGGGGAAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGGTGGCCGAG 1380
DB 1351 AGGACGACAGAGGGGAAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGGTGGCCGAG 1410
QY 1381 ACTGAGCCTTGAAGGCTGATCTTGGAGATGTGAGAACCCAGCCAGAGGCACTTGAGGG 1440
DB 1411 ACTGAGCCTTGAAGGCTGATCTTGGAGATGTGAGAACCCAGCCAGAGGCACTTGAGGG 1470
QY 1441 GGAGCCGGTAACTGCTCTGCTGCTCATTTAGCCACTTCTTTACTGCGCAAGAAATT 1500
DB 1471 GGAGCCGGTAACTGCTCTGCTGCTCATTTAGCCACTTCTTTACTGCGCAAGAAATT 1530
QY 1501 TTTTAAATTAATATTATTATAT 1522
DB 1531 TTTTAAATTAATATTATTATAT 1552

RESULT 7
ABLe2179
ID ABLe2179 standard; DNA; 1552 BP.
XX
AC ABLe2179;
XX
DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:516.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX gene; etc.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231313P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236642P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.

PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 516; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in (I)
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABLe1664
CC to ABLe10110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGGATGCTCCCTGTCGCCAGCCCTGGCTCCCTGTGATCCCGGCC 60
DB 31 ACAGTCAGCGGATGCTCCCTGTCGCCAGCCCTGGCTCCCTGTGATCCCGGCC 90
QY 61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTCTTCTGATGCTGCTCAT 120
DB 91 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCGAGAGTTCCTCCCGGATGCAAGATTTCCCTTGGAGAGGCTCTTCTGGGAA 180
DB 151 CCCGAGAGTTCCTCCCGGATGCAAGATTTCCCTTGGAGAGGCTCTTCTGGGAA 210
QY 181 GATGACCCACTGGGGGAGAGAGATCTGCGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGGGAGAGAGATCTGCGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 271 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGGAAGTGTGAGAGATCTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGGAAGTGTGAGAGATCTACTGTT 390
QY 361 GAGGCTCTGAGAGATCTCAAGAACCCAGATTAATGCCCACAGGAGCAAAAGGGGAT 420

Db 391 GAGGCTCTGGAGATCTTCAAGAACCCGAGATTAATGCTCCAGAGGAGCAAGAGGGGAT 450
 Qy 421 GACGAGAGTCATTGGGCTATGAGAGCGAACCCGCTGGCCCGGGGTGTCCGAGCTGC 480
 Db 451 GACGAGAGTCATTGGGCTATGAGAGCGAACCCGCTGGCCCGGGGTGTCCGAGCTGC 510
 Qy 481 GGGGGGCTTCCAGTCCCGGTGATATCCGCCCCAGCTGGCCGCTTCTGGCCGGCC 540
 Db 511 GGGGGGCTTCCAGTCCCGGTGATATCCGCCCCAGCTGGCCGCTTCTGGCCGGCC 570
 Qy 541 CTGGCCCCCTGGAACTCTGGGCTTCCAGCTCCGCGCTCCAGAACTGGGCTGGCC 600
 Db 571 CTGGCCCCCTGGAACTCTGGGCTTCCAGCTCCGCGCTCCAGAACTGGGCTGGCC 630
 Qy 601 AACATGGCCACAGTGTGCACTGACCTGCTCTGGGCTAGAGATGGCTGTGGGTCC 660
 Db 631 AACATGGCCACAGTGTGCACTGACCTGCTCTGGGCTAGAGATGGCTGTGGGTCC 690
 Qy 661 GGGGGGAGTACCGGGCTTGGAGCTGTGCACTGTGCACTGGGGGGCTGCAAGTGTCCGGCC 720
 Db 691 GGGGGGAGTACCGGGCTTGGAGCTGTGCACTGTGCACTGGGGGGCTGCAAGTGTCCGGCC 750
 Qy 721 TCGGAGCACTGTGGAAGGCCACGCTTCCCTGCGAGATCCAGTGGTTCACTCAAC 780
 Db 751 TCGGAGCACTGTGGAAGGCCACGCTTCCCTGCGAGATCCAGTGGTTCACTCAAC 810
 Qy 781 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGGCGCCGAGAGGCTGGCGGTGGCC 840
 Db 811 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGGCGCCGAGAGGCTGGCGGTGGCC 870
 Qy 841 GCTTTCTGGAAGAGGGCCCGAGAAACAGTGCTATGACAGTGTGTCTGTGCTGG 900
 Db 871 GCTTTCTGGAAGAGGGCCCGAGAAACAGTGCTATGACAGTGTGTCTGTGCTGG 930
 Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGTCAATATCTCACTC 960
 Db 931 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGGTCCAGAGTCAATATCTCACTC 990
 Qy 961 CTGGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTGTGACTACCGCCCTGT 1020
 Db 991 CTGGCTCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTGTGACTACCGCCCTGT 1050
 Qy 1021 GCCCAGGGGTGATGAGCTGATGTTTACAGACAGTGAATGCTAGTGAAGAGCTC 1080
 Db 1051 GCCCAGGGGTGATGAGCTGATGTTTACAGACAGTGAATGCTAGTGAAGAGCTC 1110
 Qy 1081 CACACCTCTCTGACACCTGTGGGAGCTGTGTACTCTGGCTACAGCTGAATCTCCGA 1140
 Db 1111 CACACCTCTCTGACACCTGTGGGAGCTGTGTACTCTGGCTACAGCTGAATCTCCGA 1170
 Qy 1141 GGGAGGAGCTTTGAAATGAGGAGTGAATGAGGCTCTTCCCTGCTGAGTGAACAGC 1200
 Db 1171 GGGAGGAGCTTTGAAATGAGGAGTGAATGAGGCTCTTCCCTGCTGAGTGAACAGC 1230
 Qy 1201 AGTCTCTGGGGCTGAGGCACTGATCCAGTGAATTCCTGCTGGCTGAGTGAATCTCA 1260
 Db 1231 AGTCTCTGGGGCTGAGGCACTGATCCAGTGAATTCCTGCTGGCTGAGTGAATCTCA 1290
 Qy 1261 GGCCTGTGTTTGGCTCTCTTTTCTGTACACAGCGTCCGCTTCTTGTGAGATGAGA 1320
 Db 1291 GGCCTGTGTTTGGCTCTCTTTTCTGTACACAGCGTCCGCTTCTTGTGAGATGAGA 1350
 Qy 1321 AGGCGAGCAGAAAGGGGAGCCAAAGGGGGTGTGACTACCGCCGAGAGAGTGAAGCCGAG 1380
 Db 1351 AGGCGAGCAGAAAGGGGAGCCAAAGGGGGTGTGACTACCGCCGAGAGAGTGAAGCCGAG 1410
 Qy 1381 ACTGAGGCTTGAAGGCTGATCTTGTGAGATGTTGAGAGCCAGAGAGGATCTGAAGG 1440
 Db 1411 ACTGAGGCTTGAAGGCTGATCTTGTGAGATGTTGAGAGCCAGAGAGGATCTGAAGG 1470
 Qy 1441 GGAGCCGGTAACTGTCTGTCTGTCTATATGCACTTCTTTTAACTGGCAGAAATTT 1500

Db 1471 GGAGCCGGTAACTGTCTGTCTGTCTATTAATGACACTTCTTTAACTGCCAGAAATTT 1530
 Qy 1501 TTTTAAATTAATATTTTAAAT 1522
 Db 1531 TTTTAAATTAATATTTTAAAT 1552
 RESULT 8
 ABL65416
 ID ABL65416 standard; DNA; 1552 BP.
 XX
 AC ABL65416;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:3753.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
 KW gene; ds.
 OS Homo sapiens.
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US010838.
 XX
 PR 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0231133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 22-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237112P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237588P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX

PA (AVAL-) AVALON PHARM.

PI	Young PE,	Augustus M,	Carter KC,	Ebner R,	Endress G,	Horrigan S,
PI	Soppet DR,	Weaver Z,				

DR WPI; 2002-188264/24.

Pr Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 3753; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytoskeletal activity and can be used in gene therapy. M1 can be used for screening anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1522;	DB 6;	Length 1552;
-------------	---------	-------------	-------	--------------

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAGTCAAGCCGATAGGCTTCCCTGTGCCCCAGCCCTTGCTCTCTTGTGAATCCGGGCC	60
Db	31	ACAGTCAAGCCGATAGGCTTCCCTGTGCCCCAGCCCTTGCTCTCTTGTGAATCCGGGCC	90
QY	61	CCTGTCCAGGCTCACTGTGCACTGCGTGTGCACTGCTGTTCTGATGCTTCAT	120
Db	91	CCTGTCCAGGCTCACTGTGCACTGCGTGTGCACTGCTGTTCTGATGCTTCAT	150
QY	121	CCCCAGAGGTTCGCCCGATGCAAGAGATTCCCCCTTGAGAGAGGCTCTTCTGGAGAA	180
Db	151	CCCCAGAGGTTCGCCCGATGCAAGAGATTCCCCCTTGAGAGAGGCTCTTCTGGAGAA	210
QY	181	GATGACCCACTGGGCGAGAGAGATCTGCCAAGTGAAGAGATTCAACCAAGAGAGAGAT	240
Db	211	GATGACCCACTGGGCGAGAGAGATCTGCCAAGTGAAGAGATTCAACCAAGAGAGAGAT	270
QY	241	CCACCCGGAGAGAGAGATTTACTCTGAGAGAGAGATCTTACTGGAAGAGAGATTTACT	300
Db	271	CCACCCGGAGAGAGAGATTTACTCTGAGAGAGAGATTTACTGGAAGAGAGATTTACT	330
QY	301	GAGTTAAGCCCTAAATCAGAAAGAGGGCTCCCTGAAATTTAGAGATCTACTACTGT	360
Db	331	GAGTTAAGCCCTAAATCAGAAAGAGGGCTCCCTGAAATTTAGAGATTTACTACTGT	390
QY	361	GAGGCTCTGAGAGATCTTCAAGAACCCCAAGATTATGCCCCAGAGGCAAAAGAGGGAT	420
Db	391	GAGGCTCTGAGAGATCTTCAAGAACCCCAAGATTATGCCCCAGAGGCAAAAGAGGGAT	450
QY	421	GACCAAGATCATTTGGCGCTATGAGAGCGAACCCGCCCTTGACCCTCGGGTGTCCCAAGCTGC	480
Db	451	GACCAAGATCATTTGGCGCTATGAGAGCGAACCCGCCCTTGACCCTCGGGTGTCCCAAGCTGC	510
QY	481	GCGGGCGGCTTCCAATCCCCGGTGGATATCCGCCCCCACTGGCGGCTTTTTCGCCGGGC	540
Db	511	GCGGGCGGCTTCCAATCCCCGGTGGATATCCGCCCCCACTGGCGGCTTTTTCGCCGGGC	570

QY	541	CTGGGCCCCCGGAACTCTGGGGCTTCCAGCTCCGCGCTCCGAAACCTGGCGCTGGCG	600
Db	571	CTGGGCCCCCGGAACTCTGGGGCTTCCAGCTCCGCGCTCCGAAACCTGGCGCTGGCG	630
QY	601	AACATGGCCACAGTGTGCACTGACCTGCGCTCTGGGCTAGAGATGGCTCTGGGCTCC	660
Db	631	AACATGGCCACAGTGTGCACTGACCTGCGCTCTGGGCTAGAGATGGCTCTGGGCTCC	690
QY	661	GGGCGGGAGTACCGGGCTCTGCACTGTCATCTGCACTGGGGGGCTGCAAGTCTGTCGGGC	720
Db	691	GGGCGGGAGTACCGGGCTCTGCACTGTCATCTGCACTGGGGGGCTGCAAGTCTGTCGGGC	750
QY	721	TGGAGGACACGTGTGGAAAGGCACTGTTCCCTGCGGATCCAGATCCAGTGTCACTCAGC	780
Db	751	TGGAGGACACGTGTGGAAAGGCACTGTTCCCTGCGGATCCAGATCCAGTGTCACTCAGC	810
QY	781	ACCGCTTTGGCAAGTGTGACAGAGGCTTTGGGGGCGCCGGAGGCGCTGGCGTGTGGCC	840
Db	811	ACCGCTTTGGCAAGTGTGACAGAGGCTTTGGGGGCGCCGGAGGCGCTGGCGTGTGGCC	870
QY	841	GCCTTTCTGGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCACTTGTCTGTCTGCTTG	900
Db	871	GCCTTTCTGGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCACTTGTCTGTCTGCTTG	930
QY	901	GAAGAAATCGCTGAGGAAGGCTCAGAGCTCAGGCTCCAGGACTGAGCATATCTGCACTC	960
Db	931	GAAGAAATCGCTGAGGAAGGCTCAGAGCTCAGGCTCCAGGACTGAGCATATCTGCACTC	990
QY	961	CTGGCTCTGCACTTCAAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACGCGCTGT	1020
Db	991	CTGGCTCTGCACTTCAAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACGCGCTGT	1050
QY	1021	GCCAGAGGTGTCACTGGACTGTGTGTTAAACCAACAATGTATGCTGAATGCTTAACCACTC	1080
Db	1051	GCCAGAGGTGTCACTGGACTGTGTGTTAAACCAACAATGTATGCTGAATGCTTAACCACTC	1110
QY	1081	CACACCCCTCTGCAACACCTGTGGGGAAGCTGTGACTCTCGGCTACAGCTGAATCTTCCGA	1140
Db	1111	CACACCCCTCTGCAACACCTGTGGGGAAGCTGTGACTCTCGGCTACAGCTGAATCTTCCGA	1170
QY	1141	GCGACGACGCTTTGAATGGGCGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGAACGAC	1200
Db	1171	GCGACGACGCTTTGAATGGGCGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGAACGAC	1230
QY	1201	AGTCTCGGGGTGCTGAGGCGAGTCCAGTGAATTCCTGCGCTGGCTGCTGAGATCTCTA	1260
Db	1231	AGTCTCGGGGTGCTGAGGCGAGTCCAGTGAATTCCTGCGCTGGCTGCTGAGATCTCTA	1290
QY	1261	GCCCTGTTTTGGGCTCTCTTTTGTCTGTCAACAGGCTCGGCTTCTTGTGTGAGANTGAGA	1320
Db	1291	GCCCTGTTTTGGGCTCTCTTTTGTCTGTGTCAACAGGCTCGGCTTCTTGTGTGAGANTGAGA	1350
QY	1321	AGGCAACACAGAAAGGGGAACCAAAAGGGGGTGTGACTACCGCCACAGAGAGTACCGAG	1380
Db	1351	AGGCAACACAGAAAGGGGAACCAAAAGGGGGTGTGACTACCGCCACAGAGAGTACCGAG	1410
QY	1381	ACTGAGGCTTGAAGGCTGAGTCTTGGAGATGTGAGAAAGCAGGACAGAGGATCTGAGGG	1440
Db	1411	ACTGAGGCTTGAAGGCTGAGTCTTGGAGATGTGAGAAAGCAGGACAGAGGATCTGAGGG	1470
QY	1441	GAGCGGGTAACTGTCTGTCTGCTCAATTAATGCACTTCTCTTTTAACTGTCAAGAAAT	1500
Db	1471	GAGCGGGTAACTGTCTGTCTGCTCAATTAATGCACTTCTCTTTTAACTGTCAAGAAAT	1530
QY	1501	TTTTTAAATTAATTTTAAAT 1522	
Db	1531	TTTTTAAATTAATTTTAAAT 1552	

RESULT 9
ABL68346
ID ABL68346 standard; DNA; 1552 BP
XX

AC ABL68346;
XX
XX 15-MAY-2002 (first entry)
XX
XX Kidney cancer related gene sequence SEQ ID NO:6683.
DE
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; da.
XX
XX Homo sapiens.
OS
XX
XX WO200194629-A2.
PN
XX
XX 13-DEC-2001.
PD
XX
XX 30-MAY-2001; 2001WO-US010836.
PF
XX
XX 05-JUN-2000; 2000US-0209473P.
PR
XX 05-JUN-2000; 2000US-0209531P.
PR
XX 18-SEP-2000; 2000US-0233133P.
PR
XX 18-SEP-2000; 2000US-0233617P.
PR
XX 20-SEP-2000; 2000US-0234009P.
PR
XX 20-SEP-2000; 2000US-0234034P.
PR
XX 20-SEP-2000; 2000US-0234052P.
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XX 22-SEP-2000; 2000US-0234509P.
PR
XX 22-SEP-2000; 2000US-0234567P.
PR
XX 25-SEP-2000; 2000US-0234923P.
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XX 25-SEP-2000; 2000US-0234924P.
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XX 25-SEP-2000; 2000US-0235077P.
PR
XX 25-SEP-2000; 2000US-0235082P.
PR
XX 25-SEP-2000; 2000US-0235134P.
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XX 25-SEP-2000; 2000US-0235280P.
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XX 26-SEP-2000; 2000US-0235637P.
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XX 27-SEP-2000; 2000US-0235711P.
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XX 27-SEP-2000; 2000US-0235720P.
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XX 27-SEP-2000; 2000US-0235840P.
PR
XX 27-SEP-2000; 2000US-0235863P.
PR
XX 28-SEP-2000; 2000US-0236028P.
PR
XX 28-SEP-2000; 2000US-0236032P.
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XX 28-SEP-2000; 2000US-0236033P.
PR
XX 28-SEP-2000; 2000US-0236034P.
PR
XX 28-SEP-2000; 2000US-0236109P.
PR
XX 28-SEP-2000; 2000US-0236111P.
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XX 29-SEP-2000; 2000US-0236842P.
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XX 29-SEP-2000; 2000US-0236891P.
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XX 02-OCT-2000; 2000US-0237172P.
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XX 02-OCT-2000; 2000US-0237173P.
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XX 02-OCT-2000; 2000US-0237278P.
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XX 02-OCT-2000; 2000US-0237294P.
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XX 02-OCT-2000; 2000US-0237295P.
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XX 02-OCT-2000; 2000US-0237316P.
PR
XX 03-OCT-2000; 2000US-0237425P.
PR
XX 03-OCT-2000; 2000US-0237598P.
PR
XX 03-OCT-2000; 2000US-0237604P.
PR
XX 03-OCT-2000; 2000US-0237606P.
PR
XX 03-OCT-2000; 2000US-0237608P.
PR
XX 01-NOV-2000; 2000US-0244867P.
PR
XX 01-NOV-2000; 2000US-0245084P.
XX
XX
XX (AVALON) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, and determining a change
XX in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 6683; 44bp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX
XX Sequence 1552 bp; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 100.0%; Score 1552; DB 6; Length 1552;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTACGCGCATGCTGCTCCCTGTGCCCCGAGCCCTGCTGCTGTTGATCCGGCC 60
DB 31 ACAGTACGCGCATGCTGCTCCCTGTGCCCCGAGCCCTGCTGCTGTTGATCCGGCC 90
QY 61 CCGTCTCCAGGCGCTCACTGTCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCAT 120
DB 91 CCGTCTCCAGGCGCTCACTGTCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCAT 150
QY 121 CCCAGAGGTTGCCCGGATCAGAGAGATTCCTGTCGAGAGAGGCTCTTGGGGAA 180
DB 151 CCCAGAGGTTGCCCGGATCAGAGAGATTCCTGTCGAGAGAGGCTCTTGGGGAA 210
QY 181 GATGACCACTGCGCGAGAGAGATTCCTGTCGAGAGAGATTCCTGTCGAGAGAGAT 240
DB 211 GATGACCACTGCGCGAGAGAGATTCCTGTCGAGAGAGATTCCTGTCGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATTCCTGTCGAGAGAGATTCCTGTCGAGAGAGATTCCT 300
DB 271 CCACCCGAGAGAGAGATTCCTGTCGAGAGAGATTCCTGTCGAGAGAGATTCCT 330
QY 301 GAAGTTAAGCTTAATATGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 360
DB 331 GAAGTTAAGCTTAATATGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTT 390
QY 361 GAGGCTCTGAGATCTCTCAAGAACCCCAAGATATATGCCCAAGGCAAGAGAGGAT 420
DB 391 GAGGCTCTGAGATCTCTCAAGAACCCCAAGATATATGCCCAAGGCAAGAGAGGAT 450
QY 421 GACCAAGTCAATGAGGCTATGAGAGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
DB 451 GACCAAGTCAATGAGGCTATGAGAGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 510
QY 481 GCGGCGGCTTCCAGTCCCGGATGATATCCGCCCAAGCTGCGGCTTCTGCGCGGCGC 540
DB 511 GCGGCGGCTTCCAGTCCCGGATGATATCCGCCCAAGCTGCGGCTTCTGCGCGGCGC 570
QY 541 CTGCGCGGCTTCCAGTCCCGGATGATATCCGCCCAAGCTGCGGCTTCTGCGCGGCGC 600
DB 571 CTGCGCGGCTTCCAGTCCCGGATGATATCCGCCCAAGCTGCGGCTTCTGCGCGGCGC 630
QY 601 AACATGCGCAAGTATGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 631 AACATGCGCAAGTATGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
QY 661 GGGGCGGAGTACCGGGCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 720
DB 691 GGGGCGGAGTACCGGGCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 750

QY	721	TCGAGAGCA	CATGTGAAAGGCCACCGTTTCCCTGCGAGATCAAGTGGTTCACTCAGC	780			
Db	751	TGGAGCA	CACCTGTGAAAGCCACCGTTTCCCTGCGAGATCAAGTGGTTCACTCAGC	810			
QY	781	ACCGCCTT	YGCAGAGTTGACAGAGCCCTTGGGGCCGCCGGAGGCGCTGGCCGTGTGGCC	840			
Db	811	ACCGCCTT	YGCAGAGTTGACAGAGCCCTTGGGGCCGCCGGAGGCGCTGGCCGTGTGGCC	870			
QY	841	GCCCTT	CTGAGAGAGGGCCCGAAGAAAACAATGCCCTATGACAGTTGCTGTCTGCTTG	900			
Db	871	GCCCTT	CTGAGAGAGGGCCCGAAGAAAACAATGCCCTATGACAGTTGCTGTCTGCTTG	930			
QY	901	GAAAGAA	TGCTGAGAAAGGCTCAGAGCTCAGGATCCGAGAGCTGAGATATCTGCACTC	960			
Db	931	GAAAGAA	TGCTGAGAAAGGCTCAGAGACTCAGGATCCGAGAGCTGAGATATCTGCACTC	990			
QY	961	CTGCCC	CTGTGACTTGACCGCTACTTCCATATGAGGGGCTCTTGACTACAACCGCCCTGT	1020			
Db	991	CTGCCC	CTGTGACTTGACCGCTACTTCCATATGAGGGGCTCTTGACTACAACCGCCCTGT	1050			
QY	1021	GCCGAG	GGTGTATCTGGACTGTGTGTTAAACAGACAGTATGCTGAGTGTGAAGAGCTC	1080			
Db	1051	GCCGAG	GGTGTGTATCTGGACTGTGTGTTAAACAGACAGTATGCTGAGTGTGAAGAGCTC	1110			
QY	1081	CACACCT	CTCTGACACCGCTGAGGAGACCTGGTGACTCCGGCTACACTGAACTTCCGA	1140			
Db	1111	CACACCT	CTCTGACACCGCTGTGGAGACCTGGTGACTCTGGCTACACTGAACTTCCGA	1170			
QY	1141	GCGAGCA	GACCTTGAATGGGCGAGTATGAGGCCCTCTCCCTGCTGAGTGGACAGC	1200			
Db	1171	GCGAGCA	GACCTTGAATGGGCGAGTATGAGGGCTCTCTCCCTGCTGAGTGGACAGC	1230			
QY	1201	AGTCT	CGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGTGGCTGTGTGAATCTTA	1260			
Db	1231	AGTCT	CGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGTGGCTGTGTGAATCTTA	1290			
QY	1261	GCCCTG	TTTTTGGGCTCCCTTTTGTCTGTACACAGCGTCGCGGTTCTTGTGCAATGAGA	1320			
Db	1291	GCCCTG	TTTTTGGGCTCCCTTTTGTCTGTACACAGCGTCGCGGTTCTTGTGCAATGAGA	1350			
QY	1321	AGGCA	GACAGAGGGGAAACCAAGGGGGTGTGACTACCGCCACGACAGATGCCGAG	1380			
Db	1351	AGGCA	GACAGAGGGGAAACCAAGGGGGTGTGAGCTACCGCCACGACAGATGCCGAG	1410			
QY	1381	ACTG	AAGCTTGAAGGCTGAGCTGTGATTTTGAGAAATGTGAGAACCCAGCCAGAGCATCTGAGG	1440			
Db	1411	ACTG	AAGGCTTGAAGGCTGTGATTTTGAGAAATGTGAGAACCCAGCCAGAGCATCTGAGG	1470			
QY	1441	GAGG	CGGTAACTGTCTGTCTCTGCTCATTAATGCACTTCTTTTAACTGCAAGAAATT	1500			
Db	1471	GAGG	CGGTAACTGTCTGTCTCTGCTCATTAATGCACTTCTTTTAACTGCAAGAAATT	1530			
QY	1501	TTTTAA	ATAAATTTTAAAT 1522				
Db	1531	TTTTAA	ATAAATTTTAAAT 1552				
RESULT 10							
ABX76385							
ID	ABX76385	standard; DNA; 1552 BP.					
AC	ABX76385;						
XX	02-APR-2003	(first entry)					
DE	Lung cancer-associated polynucleotide #249.						
KW	Lung cancer-associated polynucleotide; gene; de; cytostatic; emphysema;						
KW	antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;						
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;						
KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;						
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.						

XX	Unidentified.
OS	
XX	WO200286443-A2.
XX	
XX	31-OCT-2002.
XX	
XX	18-APR-2002; 2002MO-US012476.
XX	
XX	18-APR-2001; 2001US-0284770P.
XX	
XX	10-MAY-2001; 2001US-0290492P.
PR	09-NOV-2001; 2001US-0339245P.
PR	13-NOV-2001; 2001US-0350666P.
PR	29-NOV-2001; 2001US-0334370P.
PR	12-APR-2002; 2002US-0372246P.
XX	
PA	(EOSB-) EOS BIOTECHNOLOGY INC.
XX	
PI	Aziz N, Murray R;
XX	
XX	WPI; 2003-093161/08.
DR	P-PSDB; ABUS6656.
XX	
XX	Detecting a lung cancer-associated transcript in a cell from a patient
PT	for treating lung cancer, by contacting a biological sample from the
PT	patient with a polynucleotide that exhibits increased or decreased
PT	expression in lung cancer.
XX	
PS	Claim 22; Page 379-380; 453pp; English.
XX	
CC	The invention relates to a method for detecting a lung cancer-associated
CC	transcript in a cell from a patient, comprising contacting a biological
CC	sample from the patient with a polynucleotide that selectively hybridizes
CC	to a sequence that is at least 80 % identical to a gene that exhibits
CC	increased or decreased expression in lung cancer samples. Lung cancer-
CC	associated polynucleotides and polypeptides are used for identifying a
CC	compound that modulates a lung cancer-associated polypeptide, for
CC	inhibiting proliferation of a lung cancer-associated cell to treat lung
CC	cancer in a patient and for treating a mammal having lung cancer by
CC	administering a modulatory compound identified. The methods are useful
CC	for treating lung cancer, such as small cell lung cancer, non-small cell
CC	lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC	emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC	hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC	bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC	for diagnostic purposes and as targets for screening for therapeutic
CC	compounds that modulate lung cancer, such as antibodies. Sequences
CC	ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC	invention
XX	
SO	Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1522; Conservative	0; Mismatches 0; Indels 0; Gaps 0
XX	
QY	1 ACAAGTCAACCCGATGGCTCCCTTGACCCCAACCCCTGGCTCCCTGTGATCCCGGCC 60
DB	31 ACAAGTCAACCCGATGGCTCCCTTGACCCCAACCCCTGGCTCCCTGTGATCCCGGCC 90
QY	61 CCTGCTCAGGCTCACTGCTGCAACTGCTGCTGCACTGCTGCTTGATGCCCTGTCAT 120
DB	91 CCTGCTCAGGCTCACTGCTGCAACTGCTGCTGCTGCTGCTTGATGCCCTGTCAT 150
QY	121 CCCCAGAGTGTCCCGGATGAGAGGATTTCCCTTGGAGAGAGGCTCTTCTGGAGAA 180
DB	151 CCCCAGAGTGTCCCGGATGAGAGGATTTCCCTTGGAGAGAGGCTCTTCTGGAGAA 210
QY	181 GATGACCCACATGGGCGAGAGGATCTGCCACAGTGAAGAGATTTACCCAGAGAGGAGAT 240
DB	211 GATGACCCACATGGGCGAGAGGATCTGCCACAGTGAAGAGATTTACCCAGAGAGGAGAT 270
QY	241 CACCCCGAGAGAGGATCTTACCTGAGAGAGGAGATTTACTGAGAGAGGAGATTAACCT 300

Db 271 CACCCGAGAGAGAGATCTACTGAGAGAGAGATCTACTGAGAGAGAGATCTACT 330
Qy 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGT 360
Db 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGT 390
Qy 361 GAGGCTCTGAGAGATCTCAGAAACCCAGATTAATGCCACAGGAGCAAGAGAGGAT 420
Db 391 GAGGCTCTGAGAGATCTCAGAAACCCAGATTAATGCCACAGGAGCAAGAGAGGAT 450
Qy 421 GACCAAGTCATTTGGGCTATGAGAGGAGACCGGCTGGGCTGGGCTGGGCTGGG 480
Db 451 GACCAAGTCATTTGGGCTATGAGAGGAGACCGGCTGGGCTGGGCTGGGCTGGG 510
Qy 481 GCGGGGCGCTTCCAGTCCCGGCTGAGATATCCGCCCCAGCTGCGCTTCTGCGCGCC 540
Db 511 GCGGGGCGCTTCCAGTCCCGGCTGAGATATCCGCCCCAGCTGCGCTTCTGCGCGCC 570
Qy 541 CTGCGGCCCCCTGGAATCTCTGGGCTTCCAGCTCCGCGCTCCAGAACTGGGCTGGC 600
Db 571 CTGCGGCCCCCTGGAATCTCTGGGCTTCCAGCTCCGCGCTCCAGAACTGGGCTGGC 630
Qy 601 AACATAGGCAAGTGTGCAACTGACCTGCTCTGAGGCTGAGATGGGCTGAGGCTCC 660
Db 631 AACATAGGCAAGTGTGCAACTGACCTGCTCTGAGGCTGAGATGGGCTGAGGCTCC 690
Qy 661 GGGCGGAGATCCGGGCTCTGCACTGTGCACTGTGAGGAGGCTGAGGCTGAGGCT 720
Db 691 GGGCGGAGATCCGGGCTCTGCACTGTGCACTGTGAGGAGGCTGAGGCTGAGGCT 750
Qy 721 TGGAGACACATGTGAGAGGCAACCGCTTCCCTGCGGAGATCACTGCTTCACTCAGC 780
Db 751 TGGAGACACATGTGAGAGGCAACCGCTTCCCTGCGGAGATCACTGCTTCACTCAGC 810
Qy 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGCGCCCGGAGAGGCTGAGGCTTGGG 840
Db 811 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGCGCCCGGAGAGGCTGAGGCTTGGG 870
Qy 841 GCGCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGACAGTGTCTGCTGCT 900
Db 871 GCGCTTTCTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGACAGTGTCTGCTGCT 930
Qy 901 GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGCTCCGAGCTGAGCACTACTGCACTC 960
Db 931 GAAAGAAATGCTGAGAGAGGCTCAGAGATCAGGCTCCGAGCTGAGCACTACTGCACTC 990
Qy 961 CTGCGCTCTGACTTACGCGCTACTTCAATATGAGAGGCTCTGACTACACGCGCTGT 1020
Db 991 CTGCGCTCTGACTTACGCGCTACTTCAATATGAGAGGCTCTGACTACACGCGCTGT 1050
Qy 1021 GCGCAGGGTGTCACTGGAATGTTTAAACAGACAGTATGCTGATGAGCACTGCTC 1080
Db 1051 GCGCAGGGTGTCACTGGAATGTTTAAACAGACAGTATGCTGATGAGCACTGCTC 1110
Qy 1081 CACACCTCTCTGACACCTGTGGGAGCTGTGAGCTCTGCGCTTCACTGAGTAACTCCGA 1140
Db 1111 CACACCTCTCTGACACCTGTGGGAGCTGTGAGCTCTGCGCTTCACTGAGTAACTCCGA 1170
Qy 1141 GCGAGCGAGCTTTGATATGAGGAGGAGTATGAGGCTCTCTCTCTGAGTATGAGCAGC 1200
Db 1171 GCGAGCGAGCTTTGATATGAGGAGGAGTATGAGGCTCTCTCTCTGAGTATGAGCAGC 1230
Qy 1201 AATCTCTGGGCTGCTGAGCAGCACTGCAAGTAACTCTGCTGCTGCTGCTGCTGCT 1260
Db 1231 AATCTCTGGGCTGCTGAGCAGCACTGCAAGTAACTCTGCTGCTGCTGCTGCTGCT 1290
Qy 1261 GCGCTGCTTTTGGCTCTCTTTTGGCTGCTCAGCAGAGTGGCTTCTTGTGAGATGAGA 1320
Db 1291 GCGCTGCTTTTGGCTCTCTTTTGGCTGCTCAGCAGAGTGGCTTCTTGTGAGATGAGA 1350
Qy 1321 AGGAGCACAAGAGGAGAAACAAGGGGCTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380

Db 1351 AGGAGCACAAGAGGAGAAACAAGGGGCTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410
Qy 1381 ACTGAGGCTTGAAGGCTGATCTTGGAGATGTGAGAGCCAGCCAGGCACTGAGAGG 1440
Db 1411 ACTGAGGCTTGAAGGCTGATCTTGGAGATGTGAGAGCCAGCCAGGCACTGAGAGG 1470
Qy 1441 GAGCGGCTTAACTGCTCTGCTCTGCTCACTTATGCACTTCTTTTAACTGCCAGAAAT 1500
Db 1471 GAGCGGCTTAACTGCTCTGCTCTGCTCACTTATGCACTTCTTTTAACTGCCAGAAAT 1530
Qy 1501 TTTTAAATTAATTTTAAAT 1522
Db 1531 TTTTAAATTAATTTTAAAT 1552
RESULT 11
ABX76124
ID ABX76124 standard; DNA; 1552 BP.
XX
AC ABX76124;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #1.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
XX
PR 10-MAY-2001; 2001US-0290492P.
XX
PR 09-NOV-2001; 2001US-0339245P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 29-NOV-2001; 2001US-0334370P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOSB-) BOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
XX
P-PBDB; AB056408.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 189; 453p; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention

Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AAGACGAGCGGAGTGCCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCG 60
DB 31 AAGACGAGCGGAGTGCCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCCGGCG 90
QY 61 CCTGCTCCAGGCTCACTGTGCAACTGTCTGTCACTGTCTGTCTGTCTGTCTGTCA 120
DB 91 CCTGCTCCAGGCTCACTGTGCAACTGTCTGTCACTGTCTGTCTGTCTGTCTGTCA 150
QY 121 CCCGAGAGGTTGCCCCGAGTGCAGAGAGATTTCCCTTGGAGAGAGGCTTTCTGGGAA 180
DB 151 CCCGAGAGGTTGCCCCGAGTGCAGAGAGATTTCCCTTGGAGAGAGGCTTTCTGGGAA 210
QY 181 GATGACCCACTGGGCGAGAGAGATCTGCCAGAGAGAGAGATTTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGCGAGAGAGATCTGCCAGAGAGAGAGATTTCAACCCAGAGAGAGAT 270
QY 241 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
DB 271 CCAACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTACCTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTACCTACTGTT 390
QY 361 GAGGCTCCCTGAGAGATCTCTAAGAACCCCGAGATTAATGCCACAGAGAGAGAGAT 420
DB 391 GAGGCTCCCTGAGAGATCTCTAAGAACCCCGAGATTAATGCCACAGAGAGAGAGAT 450
QY 421 GACCAAGATCATTTGGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
DB 451 GACCAAGATCATTTGGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 510
QY 481 GCGGAGCGGCTTCAAGTCCCGGAGATTCGCGCCCACTGCGGCTTTCTGCGCGGCG 540
DB 511 GCGGAGCGGCTTCAAGTCCCGGAGATTCGCGCCCACTGCGGCTTTCTGCGCGGCG 570
QY 541 CTGCGGCGGCTTCAAGTCCCGGAGATTCGCGCCCACTGCGGCTTTCTGCGCGGCG 600
DB 571 CTGCGGCGGCTTCAAGTCCCGGAGATTCGCGCCCACTGCGGCTTTCTGCGCGGCG 630
QY 601 AACCAATGAGCAGATGTGCACTGACCTGAGCTCTGAGGCTGAGATGAGCTGAGGTC 660
DB 631 AACCAATGAGCAGATGTGCACTGACCTGAGCTCTGAGGCTGAGATGAGCTGAGGTC 690
QY 661 GGGCGGAGATCACGGGCTGTGCACTGACCTGCACTGAGGAGAGAGAGAGAGAGAG 720
DB 691 GGGCGGAGATCACGGGCTGTGCACTGACCTGCACTGAGGAGAGAGAGAGAGAGAG 750
QY 721 TGGAGAGCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 751 TGGAGAGCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
QY 781 ACCGCTTTGCGAGAGTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 811 ACCGCTTTGCGAGAGTTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
QY 841 GCGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 871 GCGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
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QY 901 GAAGAAATGCTGAGAGAGAGCTCAGAGACTCAGATCCAGAGACTGAGATATCTGCACTC 960
DB 931 GAAGAAATGCTGAGAGAGAGCTCAGAGACTCAGATCCAGAGACTGAGATATCTGCACTC 990
QY 961 CTGCGCTTGAATTCAGCGGCTACTTCCAAATGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 991 CTGCGCTTGAATTCAGCGGCTACTTCCAAATGAGAGAGAGAGAGAGAGAGAGAGAG 1050
QY 1021 GCCCAGGCTGATCTGAGCTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTTC 1080
DB 1051 GCCCAGGCTGATCTGAGCTGTGTTTAAACAGACAGATGATGCTGATGAGAGCTTC 1110
QY 1081 CACACCTCTGACACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1111 CACACCTCTGACACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170
QY 1141 GCGAGCAGAGCTTTGATGAGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1171 GCGAGCAGAGCTTTGATGAGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 1230
QY 1201 AGTCTCTGAGGCTGCTGAGAGAGAGATCCAGCTGAATTTCTGCTGAGCTGTGATCT 1260
DB 1231 AGTCTCTGAGGCTGCTGAGAGAGAGATCCAGCTGAATTTCTGCTGAGCTGTGATCT 1290
QY 1261 GCGCTGATTTTGGGCTCTTTTGTCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1291 GCGCTGATTTTGGGCTCTTTTGTCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
QY 1321 AGGCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1351 AGGCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
QY 1381 ACTGAGCTTGAAGGCTGATTTTGAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1411 ACTGAGCTTGAAGGCTGATTTTGAAGATGTGAGAGAGAGAGAGAGAGAGAGAGAG 1470
QY 1441 GAGAGCGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1471 GAGAGCGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
QY 1501 TTTTAAATTAATTAATTAATTAAT 1522
DB 1531 TTTTAAATTAATTAATTAATTAAT 1552
```

RESULT 12
AD89343
ID AD89343 standard; DNA; 1552 BP.
XX
AC AD89343;
XX
DT 11-MAR-2004 (first entry)
XX
DB Cancer detection method related gene #6.
XX
KW ds; cancer; gene expression;
KM estrogen receptor-positive invasive breast cancer.
OS Homo sapiens.
PN W02003078662-A1.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007713.
XX
PR 13-MAR-2002; 2002US-0364890P.
XX
PR 18-SEP-2002; 2002US-0412049P.
XX
PA (GENO-) GENOMIC HEALTH INC.
XX
PI Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX

DR MPI: 2003-767536/72.

XX Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.

XX Disclosure; SEQ ID NO 291; 198bp; English.

XX The invention relates to a method of predicting clinical outcome for a
CC patient diagnosed with cancer by determining the expression level of one
CC or more genes, or their expression products, selected from p53BP2,
CC cathepsin B, cathepsin L, K167/MiB1, and thymidine kinase in a cancer
CC tissue obtained from the patient, normalized against control gene(s), and
CC compared to the amount found in a reference cancer tissue set. The
CC specification also discloses an array comprising polynucleotides
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, SKI5, CEGP1, K1-
CC 67, GSTM1, CA9, PR, BRC3, NME1, SURV, GATM3, TFR3, YB-1, DPYD, GSTM4,
CC RPS6KB1, Srs, Chk1, ID1, BSR1, p27, CNB1, XIAP, Chk2, CDC25B, IGFBP,
CC AK05699, PI3K2A, TGBB3, BAG1, CYP3A4, BPCAM, VEGFR, p21, hENT1, MISP1,
CC HNF3A, NFKBp65, BRC2, EGFR, TKI, VDR, Contig51037, pENT1, EPHX1, IFA,
CC CDH1, HIF1c, IGFBP3, CTSE, Her2 and DIABLO, immobilized on a solid
CC surface. The methods are useful for predicting clinical outcome for a
CC patient diagnosed with cancer, classifying cancer, and predicting the
CC likelihood of long-term survival of a breast cancer patient, or a patient
CC diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC positive invasive breast cancer. This sequence corresponds to a gene
CC sequence whose expression is detected by the method of the invention.

XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 10; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGTCAGCGGATGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCGAGC 60
DB 31 ACAAGTCAGCGGATGCTCCCTGTCGCCAGCCCTGCTCCCTGTTGATCCGAGC 90
QY 61 CCTGCTCCAGGCTCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 91 CCTGCTCCAGGCTCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCT 150
QY 121 CCCGAGGCTTCCCGGATGAGAGGATTCCTCCCTGAGAGGAGCTCTTCCGAGAA 180
DB 151 CCCGAGGCTTCCCGGATGAGAGGATTCCTCCCTGAGAGGAGCTCTTCCGAGAA 210
QY 181 GATGACCCACTGAGGAGGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGAGGAGGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
QY 241 CCAACCCGAGAGAGAGATTTACCTGGAGAGAGATCTTCTGGAGAGAGATTTACCT 300
DB 271 CCAACCCGAGAGAGAGATTTACCTGGAGAGAGATCTTCTGGAGAGAGATTTACCT 330
QY 301 GAAAGTTAAGCTTAATCAGAAGAGAGGCTCCCTGAAGTTAAGAGATTTACTACTGT 360
DB 331 GAAAGTTAAGCTTAATCAGAAGAGAGGCTCCCTGAAGTTAAGAGATTTACTACTGT 390
QY 361 GAGGCTCTGAGAGATCTTCAAGAACCCAGAAATTAATGCCACAGGAGCAAAAGAGAGAT 420
DB 391 GAGGCTCTGAGAGATCTTCAAGAACCCAGAAATTAATGCCACAGGAGCAAAAGAGAGAT 450
QY 421 GACCGAGATCATTTGGGCTTATGAGAGCGACCCGCTTGAGCCCGGGGTGCTCCAGCTGAC 480
DB 451 GACCGAGATCATTTGGGCTTATGAGAGCGACCCGCTTGAGCCCGGGGTGCTCCAGCTGAC 510
QY 481 GCGGCGCGCTTCCAGTCCCGGAGATATCGGCCCCAGCTGCGGCTTCCGCGGCGC 540
DB 511 GCGGCGCGCTTCCAGTCCCGGAGATATCGGCCCCAGCTGCGGCTTCCGCGGCGC 570
QY 541 CTGCGCCCGCTTGAAATCTCTGAGGCTTCCAGCTCCGCGGCTTCCAGAACTGCGGCTGCGC 600
DB 571 CTGCGCCCGCTTGAAATCTCTGAGGCTTCCAGCTCCGCGGCTTCCAGAACTGCGGCTGCGC 630

QY 601 AACAAATGCGCACTGTGCAACTGACCTGCTCTGAGGCTTGAAGATGAGCTTGGGCTCC 660
DB 631 AACAAATGCGCACTGTGCAACTGACCTGCTCTGAGGCTTGAAGATGAGCTTGGGCTCC 690
QY 661 GGGCGGAGATACCGGGCTCTGACAGTGCATCTGCACTGGGGGCTGCAAGTCTGTCGGAGC 720
DB 691 GGGCGGAGATACCGGGCTCTGACAGTGCATCTGCACTGGGGGCTGCAAGTCTGTCGGAGC 750
QY 721 TCGAGCACTGTGGAAGGACACCGTTTCCCTGCGAGATCACTGAGTTTCACTGACG 780
DB 751 TCGAGCACTGTGGAAGGACACCGTTTCCCTGCGAGATCACTGAGTTTCACTGACG 810
QY 781 ACCGCTTTCGCAAGTTGACGAGGCTTGGGAGGCGCCGAGAGGCTGCGGCTGTCGCC 840
DB 811 ACCGCTTTCGCAAGTTGACGAGGCTTGGGAGGCGCCGAGAGGCTGCGGCTGTCGCC 870
QY 841 GCGTTTTCGAGAGAGGCGCGGAGAGAAACAGTGCATATGAGAGCTGCTGCTGCTTG 900
DB 871 GCGTTTTCGAGAGAGGCGCGGAGAGAAACAGTGCATATGAGAGCTGCTGCTGCTTG 930
QY 901 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCAGAGACTGACATATCTGACATC 960
DB 931 GAAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTCAGAGACTGACATATCTGACATC 990
QY 961 CTGCGCTTCTGACTTCAAGCGCTTACTTCCATATATGAGGGGCTTCTGACTTCAACCGCCTGT 1020
DB 991 CTGCGCTTCTGACTTCAAGCGCTTACTTCCATATATGAGGGGCTTCTGACTTCAACCGCCTGT 1050
QY 1021 GCCAGAGGTCATCTGAGTCTGTTTAAACAGACAGTGAAGTGCATGAGAGCTC 1080
DB 1051 GCCAGAGGTCATCTGAGTCTGTTTAAACAGACAGTGAAGTGCATGAGAGCTC 1110
QY 1081 CACAACCTCTCTGACACCTGTGAGGACCTGTGATCTCTCGGCTTACAGCTGAATTCGGA 1140
DB 1111 CACAACCTCTCTGACACCTGTGAGGACCTGTGATCTCTCGGCTTACAGCTGAATTCGGA 1170
QY 1141 GCGAGCAGCCTTTGAATGAGGCGAGTGAAGGCTCTTCTGCTGAGTGAAGCAGC 1200
DB 1171 GCGAGCAGCCTTTGAATGAGGCGAGTGAAGGCTCTTCTGCTGAGTGAAGCAGC 1230
QY 1201 AGTCCTGAGGCTGCTGAGGCGAGTCAAGTCAATTCCTGCGGCTGCTGAGTCAATCTCTA 1260
DB 1231 AGTCCTGAGGCTGCTGAGGCGAGTCAAGTCAATTCCTGCGGCTGCTGAGTCAATCTCTA 1290
QY 1261 GCGCTGTTTGTGCTCTTCTTGTGCTGCAACAGCTGCGGCTCTTGTGCAAGTGAAGA 1320
DB 1291 GCGCTGTTTGTGCTCTTCTTGTGCTGCAACAGCTGCGGCTCTTGTGCAAGTGAAGA 1350
QY 1321 AGGCAAGCAGAGAGGAGAACCAAGGGGCTGTGAGCTACCGCCAGCAGAGATGCGAG 1380
DB 1351 AGGCAAGCAGAGAGGAGAACCAAGGGGCTGTGAGCTACCGCCAGCAGAGATGCGAG 1410
QY 1381 ACTGGAAGCTGAGAGCTGATCTTGAAGATGTGAAGAGCCAGGCAAGAGGATCTGAAGG 1440
DB 1411 ACTGGAAGCTGAGAGCTGATCTTGAAGATGTGAAGAGCCAGGCAAGAGGATCTGAAGG 1470
QY 1441 GAGACCGGTAACTGCTCTGCTGCTGCTCAATATGCACTTCTTTAACTGCAAGAAAT 1500
DB 1471 GAGACCGGTAACTGCTCTGCTGCTGCTCAATATGCACTTCTTTAACTGCAAGAAAT 1530
QY 1501 TTTTAAATTAATTTTATTAAT 1522
DB 1531 TTTTAAATTAATTTTATTAAT 1552

RESULT 13
ACCT72730
ID ACCT72730 standard; cDNA; 1552 BP.
XX ACCT72730;
XX
XX
DT 09-JUN-2003 (first entry)

XX DE Human cancer related protein encoding cDNA SEQ ID NO:69.
XX KW Human, cancer; diagnosis; screening; modulator; leukemia; ischemia;
XX KW heart disease; atherosclerosis; endometrios; gene; ss.
XX OS Homo sapiens.
XX PN MO2003025138-42.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WC-US029560.
XX PR 17-SEP-2001; 2001US-0323469P.
XX PR 20-SEP-2001; 2001US-0323887P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 08-FEB-2002; 2002US-0355145P.
XX PR 08-FEB-2002; 2002US-0355257P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Afar D, Aziz N, Glash KC, Hevezi PA, Mack DH, Wilson KE;
XX PI Zlotnick A;
XX DR WPI, 2003-354600/33.
XX DR P-PSDB; ABR58595.
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX PS Claim 8; Page 662; 767pp; English.
XX PS The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer in
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR58521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
XX CC atherosclerosis and endometrios. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCGCGATGCTCCCTGTCGCCCAAGCCCTGCTCCTCTGTGATCCCGGCC 60
DB 31 ACAGTCAGCGCGATGCTCCCTGTCGCCCAAGCCCTGCTCCTCTGTGATCCCGGCC 90
QY CCGTCGCCCGGCTCACTGTCGAACCTGCTGCTCACTGCTGCTTGTGATCCCTGTCAT 120
DB 61 CCGTCGCCCGGCTCACTGTCGAACCTGCTGCTCACTGCTGCTTGTGATCCCTGTCAT 150
QY CCGTCGCCCGGCTCACTGTCGAACCTGCTGCTCACTGCTGCTTGTGATCCCTGTCAT 180
DB 91 CCGTCGCCCGGCTCACTGTCGAACCTGCTGCTCACTGCTGCTTGTGATCCCTGTCAT 210
QY CCCCAAGAGGTTGCCCCGAGATGACAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGAA 180
DB 121 CCCCAAGAGGTTGCCCCGAGATGACAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGAA 210
151 CCCCAAGAGGTTGCCCCGAGATGACAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGAA 210

QY 181 GATGACCCACTGGGAGAGAGATGTCGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGAGAGAGATGTCGCCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
QY 241 CCACCCGAGAGAGAGATCTTACCTTGAGAGAGATCTTACCTTGAGAGAGATCTTACCT 300
DB 271 CCACCCGAGAGAGAGATCTTACCTTGAGAGAGATCTTACCTTGAGAGAGATCTTACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATTACTTACTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATTACTTACTGTT 390
QY 361 GAGGCTCCCTGAGATCCTCAAGAACCCCAAGTAATGCCCAAGGAGCAAAAGAGAGAT 420
DB 391 GAGGCTCCCTGAGATCCTCAAGAACCCCAAGTAATGCCCAAGGAGCAAAAGAGAGAT 450
QY 421 GACCAAGATCATTTGCGCTATATGAGAGCGACCCGCTGCGCCCGGAGTCTCCAGCCTGC 480
DB 451 GACCAAGATCATTTGCGCTATATGAGAGCGACCCGCTGCGCCCGGAGTCTCCAGCCTGC 510
QY 481 GCGGCGCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTCTGCGCGGCC 540
DB 511 GCGGCGCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTCTGCGCGGCC 570
QY 541 CTGGCGCCCTGGAATCCTCTGGGCTTCCAGCTCCCGCGCTCCCAAGACTGGCGCTGGCG 600
DB 571 CTGGCGCCCTGGAATCCTCTGGGCTTCCAGCTCCCGCGCTCCCAAGACTGGCGCTGGCG 630
QY 601 AACCAATGCGCAGATGTCAGTGAACCTGCTCCTGCTGAGTGAAGTGTGAGTCTGAGTCC 660
DB 631 AACCAATGCGCAGATGTCAGTGAACCTGCTCCTGCTGAGTGAAGTGTGAGTCTGAGTCC 690
QY 661 GGGCGGAGTACCGGCTCTGCACTGTCATCTGCACTGGGGGGCTGCAAGTGTGCGGGC 720
DB 691 GGGCGGAGTACCGGCTCTGCACTGTCATCTGCACTGGGGGGCTGCAAGTGTGCGGGC 750
QY 721 TGGGAGCACATGTCGGAAGGCGACCGTTTCCGTCGAGATCCAGTGTGTCACCTGACG 780
DB 751 TGGGAGCACATGTCGGAAGGCGACCGTTTCCGTCGAGATCCAGTGTGTCACCTGACG 810
QY 781 ACCGCTTTGCGCAGATGTCAGAGGCTGCGGCGCCGCGGAGGCTGCGCTGTTGGCC 840
DB 811 ACCGCTTTGCGCAGATGTCAGAGGCTGCGGCGCCGCGGAGGCTGCGCTGTTGGCC 870
QY 841 GCGTTTCTGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTGCTTG 900
DB 871 GCGTTTCTGAGAGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTGCTTG 930
QY 901 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGTCCCGAGACTGAGACTGATCTGACATC 960
DB 931 GAAAGAAATGCTGAGAGAGGCTCAGAGACTCAGTCCCGAGACTGAGACTGATCTGACATC 990
QY 961 CTGCCCTTGAATGAGCGGCTTCCAAATGAGAGGCTCTCTGACTACACCGCCCTGT 1020
DB 991 CTGCCCTTGAATGAGCGGCTTCCAAATGAGAGGCTCTCTGACTACACCGCCCTGT 1050
QY 1021 GCCCAAGGTCATCTGATCTGTGTTTAAACAGACAGTATGCTGATGCTGAAGCAGCTC 1080
DB 1051 GCCCAAGGTCATCTGATCTGTGTTTAAACAGACAGTATGCTGATGCTGAAGCAGCTC 1110
QY 1081 CACACCTTCTGACACCTCTGAGGAGACCTGAGTACTCTCGGCTCAAGTGAACCTTCCGA 1140
DB 1111 CACACCTTCTGACACCTCTGAGGAGACCTGAGTACTCTCGGCTCAAGTGAACCTTCCGA 1170
QY 1141 GCGAGCAGACCTTGAATGAGGAGAGTGAAGGCTCTCTGCTGCTGAGTGAAGCAGC 1200
DB 1171 GCGAGCAGACCTTGAATGAGGAGAGTGAAGGCTCTCTGCTGCTGAGTGAAGCAGC 1230
QY 1201 AGTCTCGGAGCTGTCAGGCACTGCAAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1231 AGTCTCGGAGCTGTCAGGCACTGCAAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1290

QY 1261 GCCCTGTTTGGCTCTTTTGTCTGACACGAGGTCGCTTCTTGTGATGAGA 1320
DB 1291 GCCCTGTTTGGCTCTTTTGTCTGACACGAGGTCGCTTCTTGTGATGAGA 1350
QY 1321 AGGACACAGAGAGGAGAACCAAGAGGGGTGTAGGCTACCGCCACAGAGGTAGCCGAG 1380
DB 1351 AGGACACAGAGAGGAGAACCAAGAGGGGTGTAGGCTACCGCCACAGAGGTAGCCGAG 1410
QY 1381 ACTGAGACCTGAGAGGCTGATCTTGAGAAATGTGAGAACGACGACGAGCATCTGAGG 1440
DB 1411 ACTGAGACCTGAGAGGCTGATCTTGAGAAATGTGAGAACGACGACGAGCATCTGAGG 1470
QY 1441 GAGAGCGGTACCTGCTCTGCTGCTCATATGACCATCTTCTTACTGCCAAGAAAT 1500
DB 1471 GAGAGCGGTACCTGCTCTGCTGCTCATATGACCATCTTCTTACTGCCAAGAAAT 1530
QY 1501 TTTTAAATTAATATTTATAT 1522
DB 1531 TTTTAAATTAATATTTATAT 1552

RESULT 14

ABZ7284
ID ABZ7284 standard; cDNA; 1552 BP.

XX AC ABZ7284;

XX DT 28-MAY-2003 (first entry)

XX DE Nucleotide sequence of human CA9 polypeptide.

KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
follicular development; CA9; HXB; IGFBP5; HPARP; STC1; mlg-6; SSR4;
cancer; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 43..1422
FT /tag= a
FT /product= "CA9"

XX PN WO2003010205-A1.

XX PD 06-FEB-2003.

XX PF 26-JUL-2002; 2002WO-US023786.

XX PR 26-JUL-2001; 2001US-0307600P.

XX PR 24-JUL-2002; 2002US-00201642.

XX PA (UYDU-) UNIV DUKE MEDICAL CENT.

XX PI Riglins GJ, Lal A;

XX DR WPI; 2003-239423/23.

XX DR P-PSDB; ABP9744.

XX PT Inhibiting angiogenesis for treating wound healing, retinopathy,

XX PT ischemia, inflammation, microvasculopathy, bone healing, skin

XX PT inflammation or follicular development by providing to a subject an

XX PT antisense polynucleotide.

XX PS Claim 1; Page 47; 66pp; English.

XX CC The present sequence encodes a human CA9 polypeptide. It is used in the
method of the invention. The specification describes a method modulating
angiogenesis associated with wound healing, retinopathy, ischemia,
inflammation, microvasculopathy, bone healing, skin inflammation or
follicular development. The method comprises providing to a subject HOG3,
HOG8, HOG18, CA9, HXB, IGFBP5, HPARP, STC1, mlg-6 or SSR4. The methods,
antisense polynucleotides, polypeptides and antibodies are useful for

CC treating wound healing, retinopathy, ischemia, inflammation,
microvasculopathy, bone healing, skin inflammation or follicular
development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma

XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 10; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTCAAGCCGATGAGGCTCCCTGTGAGCCGACGCTTGGCTTGTGATCCCGGC 60
DB 31 AAGTCAAGCCGATGAGGCTCCCTGTGAGCCGACGCTTGGCTTGTGATCCCGGC 90
QY 61 CTTGCTCCAGGCTCACTGTGCAACTGTGCTGCTCACTGTGCTTCTGATGCTGCTCAT 120
DB 91 CTTGCTCCAGGCTCACTGTGCAACTGTGCTGCTCACTGTGCTTCTGATGCTGCTCAT 150
QY 121 CCCCAGAGGTTGCCCGGATGAGAGGATTCGCCCTTGAGAGAGAGGCTTCTGAGGAA 180
DB 151 CCCCAGAGGTTGCCCGGATGAGAGGATTCGCCCTTGAGAGAGAGGCTTCTGAGGAA 210
QY 181 GATGACCCACTGGGCGAGAGAGATTCGCCGATGAGAGAGATTCACCCAGAGAGAGAT 240
DB 211 GATGACCCACTGGGCGAGAGAGATTCGCCGATGAGAGAGATTCACCCAGAGAGAGAT 270
QY 241 CCAACCCGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCT 300
DB 271 CCAACCCGAGAGAGAGATTCACCTGAGAGAGAGATTCACCTGAGAGAGAGATTCACCT 330
QY 301 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTGTT 360
DB 331 GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTGTT 390
QY 361 GAGGCTCTGAGAGATTCCTCAAGAACCCCAAGATTAATGCCCAAGAGCAAGAGAGAT 420
DB 391 GAGGCTCTGAGAGATTCCTCAAGAACCCCAAGATTAATGCCCAAGAGCAAGAGAGAT 450
QY 421 GACCAAGTCAATGAGGCTATGAGAGGAGCCGCGCTTGAGGCTCCCAAGCTGCG 480
DB 451 GACCAAGTCAATGAGGCTATGAGAGGAGCCGCGCTTGAGGCTCCCAAGCTGCG 510
QY 481 GCGGCGGCTTCCAGTCCCGGCTGAGATTCGCGCCCAAGCTGCGCGCTTCTGCGCGGC 540
DB 511 GCGGCGGCTTCCAGTCCCGGCTGAGATTCGCGCCCAAGCTGCGCGCTTCTGCGCGGC 570
QY 541 CTGGGCCCCCTGAAGATCTGAGGCTTCCAGGCTCCGCGCTCCAGAACTGCGGCTGCG 600
DB 571 CTGGGCCCCCTGAAGATCTGAGGCTTCCAGGCTCCGCGCTCCAGAACTGCGGCTGCG 630
QY 601 AACCAATGGCCACAGTGTGCACTGACCCCTGCTCTGAGGCTTGAAGATGCTGAGTCCC 660
DB 631 AACCAATGGCCACAGTGTGCACTGACCCCTGCTCTGAGGCTTGAAGATGCTGAGTCCC 690
QY 661 GCGGCGGAGTACCGGCGCTTGCAGCTGATTCGATCGGCGGCTGCAAGTCTGCGGCG 720
DB 691 GCGGCGGAGTACCGGCGCTTGCAGCTGATTCGATCGGCGGCTGCAAGTCTGCGGCG 750
QY 721 TCGAGGCACTGTGAGAGGCAACGTTTCCCTGCGAGATTCAGAGTGTTCACCTGAGC 780
DB 751 TCGAGGCACTGTGAGAGGCAACGTTTCCCTGCGAGATTCAGAGTGTTCACCTGAGC 810
QY 781 ACCGCTTTTGCAGAGTTGACGAGGCTTGGAGGCGCCGAGAGGCTGCGCGTGTGCGC 840
DB 811 ACCGCTTTTGCAGAGTTGACGAGGCTTGGAGGCGCCGAGAGGCTGCGCGTGTGCGC 870
QY 841 GCTTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTTATGACGTTGCTGTCTGCTTG 900
DB 871 GCTTTTCTGAGAGAGGCGCCGAGAGAAACAGTGTCTTATGACGTTGCTGTCTGCTTG 930
QY 901 GAAGAAATCGGTGAGAGGCTCAGAGACTCAGGTTCCAGAGATCATATGCACTC 960

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Db      931 GAAGAAATGCTGAGGAAAGCTCAGAGACTCAGTCCAGAGATGATATCTGCACTC 990
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Db      991 CCGCCCTGATTTAGCCGCTACTTCCAAATAGAGGGTCTTGACTACCCGCTCT 1050
Qy      1021 GCCCAGGGTGTATCTGAGCTGTGTTAAACAGACAGATGCTGAGTCTTAAGCAGCTC 1080
Db      1051 GCCCAGGGTGTATCTGAGCTGTGTTAAACAGACAGATGCTGAGTCTTAAGCAGCTC 1110
Qy      1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTCTGCTACAGTGAATCTTCGA 1140
Db      1111 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTCTGCTACAGTGAATCTTCGA 1170
Qy      1141 GGGAGCGACCTTTGAAATGGGCGAGTGAATGAGGCTCTTCCCTGCTGAGATGAGCAGC 1200
Db      1171 GGGAGCGACCTTTGAAATGGGCGAGTGAATGAGGCTCTTCCCTGCTGAGATGAGCAGC 1230
Qy      1201 AGTCTCTGGGCTGCTGAGCAGCTCAGCTGAATTCCTGCTGAGCTGCTGATCTCTA 1260
Db      1231 AGTCTCTGGGCTGCTGAGCAGCTCAGCTGAATTCCTGCTGAGCTGCTGATCTCTA 1290
Qy      1261 GGCCTGTGTTTTGGCCTCTTTTGTCTGTCAACAGGCTGCGTCTCTTGTGAGATGAGA 1320
Db      1291 GGCCTGTGTTTTGGCCTCTTTTGTCTGTCAACAGGCTGCGTCTCTTGTGAGATGAGA 1350
Qy      1321 AGGCGACAGAGAGGGGAAACCAAGGGGCTGTGAGCTTACCCGCGCAGAGAGTACCGAG 1380
Db      1351 AGGCGACAGAGAGGGGAAACCAAGGGGCTGTGAGCTTACCCGCGCAGAGAGTACCGAG 1410
Qy      1381 ACTGAGGCTTGAAGGCTGTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGGATCTGAGGG 1440
Db      1411 ACTGAGGCTTGAAGGCTGTGATCTTGGAGAAATGTGAGAGCCAGCCAGAGGATCTGAGGG 1470
Qy      1441 GGAGCCGGTACTGTCTCTCTGCTCATTATGCACTTCTTTTAATGCGAAGAAAT 1500
Db      1471 GGAGCCGGTACTGTCTCTCTGCTCATTATGCACTTCTTTTAATGCGAAGAAAT 1530
Qy      1501 TTTTAAATTAATATTTATTAAT 1522
Db      1531 TTTTAAATTAATATTTATTAAT 1552

RESULT 15
ADN39704
ID      ADN39704 standard; cDNA, 1552 BP.
XX
AC      ADN39704;
XX
DT      17-JUN-2004 (first entry)
XX
DE      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C76.
XX
KM      Human; differential expression; cancer; angiogenic disorder;
KM      fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
KM      inflammatory disease; autoimmune disease;
KM      retinal neovascularization syndrome; scarring; uterine fibroid;
KM      detection; diagnosis; prognosis; drug screening; drug targeting;
KM      wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KM      vulnery; gene therapy; vaccine; gene; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003042661-A2.
XX
PD      22-MAY-2003.
XX
PF      13-NOV-2002; 2002WO-US036810.
XX
PR      13-NOV-2001; 2001US-0350666P.
PR      21-NOV-2001; 2001US-0332464P.
PR      29-NOV-2001; 2001US-0334393P.
PR      03-DEC-2001; 2001US-0335394P.

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PR      14-DEC-2001; 2001US-0340376P.
PR      08-JAN-2002; 2002US-0347211P.
PR      10-JAN-2002; 2002US-0347349P.
PR      08-FEB-2002; 2002US-0355250P.
PR      13-FEB-2002; 2002US-0356714P.
PR      20-FEB-2002; 2002US-0359077P.
PR      29-MAR-2002; 2002US-0368809P.
PR      04-APR-2002; 2002US-0370110P.
PR      12-APR-2002; 2002US-0372246P.
PR      05-JUN-2002; 2002US-0386614P.
PR      16-JUL-2002; 2002US-0396839P.
PR      22-JUL-2002; 2002US-0397757P.
PR      22-JUL-2002; 2002US-0397845P.
PR      09-SEP-2002; 2002US-0409450P.
XX
PA      (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI      Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI      Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR      WPI; 2003-468649/44.
XX
F-PSDB; ADN39921.
XX
PT      Determining the presence or absence of a pathological cell in a patient,
PT      useful for diagnosing, prognosing or treating cancer, comprises detecting
PT      a nucleic acid in a biological sample.
XX
PS      Claim 8; SEQ ID NO C76; 1385bp; English.
XX
CC      The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC      whose expression is upregulated or downregulated in specific cancers or
CC      other diseases such as angiogenic or fibrotic disorders, and to methods
CC      of determining the presence or absence of a pathological cell in a
CC      patient by detecting a nucleic acid at least 80% identical to those of
CC      the invention or by detecting a polypeptide of the invention. The
CC      invention also relates to expression vectors and host cells comprising a
CC      nucleic acid of the invention; antibodies which specifically bind a
CC      polypeptide of the invention; use of such antibodies for drug targeting;
CC      and methods of screening for modulators of activity or expression of the
CC      polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC      antibodies and methods are useful for diagnosing, prognosing and treating
CC      cancer and other conditions such as psoriasis, ischemia, heart disease,
CC      atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC      neovascularization syndromes, scarring and uterine fibroids. They may
CC      also be useful in wound healing and in contraception. The present
CC      sequence represents a nucleic acid sequence of the invention.
XX
SQ      Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX
Query Match      100.0%; Score 1522; DB 11; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ACAGTCAGCGGATGAGTCCCTGTGAGCCAGCCCTGGCTCTCTGTGATCCCGGCC 60
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Qy      121 CCCGAGAGTGGTCCCGGATGAGAGGATTTCCCTTGGAGAGAGGCTCTTCTGGGAA 180
Db      151 CCCGAGAGTGGTCCCGGATGAGAGGATTTCCCTTGGAGAGAGGCTCTTCTGGGAA 210
Qy      181 GATGACCACTGTGGGAGAGAGATCTGCGCAGTGAAGAGATTCAACCCAGAGAGAGAT 240
Db      211 GATGACCACTGTGGGAGAGAGATCTGCGCAGTGAAGAGATTCAACCCAGAGAGAGAT 270
Qy      241 CCACCCGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATTTACT 300
Db      271 CCACCCGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATTTACT 330

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QY	301	GAAGTTAAGCTTAATCAGAGAAAGAGGGCTCTCTGAAAGTAAAGAGATCTACCTGTGTT	360
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QY	361	GAGGCTCCCGAGAGATCTCAAGAAACCCAGAAATTAATGCCCAAGGGAGCAAAAGAGGAT	420
DB	391	GAGGCTCCCGAGAGATCTCAAGAAACCCAGAAATTAATGCCCAAGGGAGCAAAAGAGGAT	450
QY	421	GACCAAGATCAATGGCGCTATGGAAGCGACCCGCCCTGGCCCCGGAGTGTCCCAAGCTGC	480
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QY	481	GGGGGCGCGTTCCAGTCCCGGGTGAATATCCGCGCCCAAGTGGCGCGCTTCGCCCGGC	540
DB	511	GGGGGCGCGTTCCAGTCCCGGGTGAATATCCGCGCCCAAGTGGCGCGCTTCGCCCGGC	570
QY	541	CTGCGCCCCCTGGAATCTCTGGAGCTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGC	600
DB	571	CTGCGCCCCCTGGAATCTCTGGAGCTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGC	630
QY	601	AACAAATGGCCACAGTGTGCACTGACCTGTCTCTGGGCTAAGAGATGGCTGTGGGTCCC	660
DB	631	AACAAATGGCCACAGTGTGCACTGACCTGTCTCTGGGCTAAGAGATGGCTGTGGGTCCC	690
QY	661	GGGCGGGAGTACCGGGCTCTGAGCTGCAATCTGCACTGGGGGGGCTGACAGTGTCCGGGC	720
DB	691	GGGCGGGAGTACCGGGCTCTGAGCTGCAATCTGCACTGGGGGGGCTGACAGTGTCCGGGC	750
QY	721	TGGAGCACACTGTGGAAGGCCACCGTTCCTGTCCAGATCAAGTGTGATCACTCAAGC	780
DB	751	TGGAGCACACTGTGGAAGGCCACCGTTCCTGTCCAGATCAAGTGTGATCACTCAAGC	810
QY	781	ACCGGCTTTCAGAGTTGACGAGGCTGTGGGGCGCCCGGAGGCGTGGCGGTGTGGGC	840
DB	811	ACCGGCTTTCAGAGTTGACGAGGCTGTGGGGCGCCCGGAGGCGTGGCGGTGTGGGC	870
QY	841	GCTTTCTGAGAGAGGCGCCCGAAGAAAACAAGTGCCTAATGAGCAATTCTGTGCTGTG	900
DB	871	GCTTTCTGAGAGAGGCGCCCGAAGAAAACAAGTGCCTAATGAGCAATTCTGTGCTGTG	930
QY	901	GAAAGAAATCGCTAGAGAAAGGCTCAGAGCTCAGGCTCCAGAGCTGGAATATCTGCACTC	960
DB	931	GAAAGAAATCGCTAGAGAAAGGCTCAGAGCTCAGGCTCCAGAGCTGGAATATCTGCACTC	990
QY	961	CTGCCCTCTGACTTCAGCCCGCTACTTCCAAATATGAGGGGTCTGTGACTTACACCGCCCTGT	1020
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DB	1051	GCCCAAGGTTGATGTGACCTGTGTTTAAACAGACAGTGAATGCTGAATGCTTAAGACGCTC	1110
QY	1081	CACACCTCTCTGACACCTGTGAGGAGCTGGTGACTCTCGGCTTACAGCTGAACCTTCGGA	1140
DB	1111	CACACCTCTCTGACACCTGTGAGGAGCTGGTGACTCTCGGCTTACAGCTGAACCTTCGGA	1170
QY	1141	GCGACGCAAGCTTTGAATGGGCGAGTGAATTGAAGCTCTCTTCCTGTGAGTGAAGCAGC	1200
DB	1171	GCGACGCAAGCTTTGAATGGGCGAGTGAATTGAAGCTCTCTTCCTGTGAGTGAAGCAGC	1230
QY	1201	AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGGTGCTGTGAGTGAATCTTA	1260
DB	1231	AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGGTGCTGTGAGTGAATCTTA	1290
QY	1261	GCCCTGATTTTGGCTCTCTTTTGTGCTGTCAACAGCGTCCGCTTCTTTGTCAGATGAGA	1320
DB	1291	GCCCTGATTTTGGCTCTCTTTTGTGCTGTCAACAGCGTCCGCTTCTTTGTCAGATGAGA	1350
QY	1321	AGGCAAGCACAAAGGGGAAACAAAGGGGGTGTGAGTACCGGCCAGACAGATGTACCGAG	1380
DB	1351	AGGCAAGCACAAAGGGGAAACAAAGGGGGTGTGAGTACCGGCCAGACAGATGTACCGAG	1410
QY	1381	ACTGAGGCTTAAGGCTGATCTTTGGAATATGTGAAAGCCAGCCAGAGGATCTGAGGG	1440

Db	1411	ACTGAGACCTTAGAGGCTCGGATCTTGGAGAAATGTGAGAGACGACCGAGGCACTGTGAGG	1470
Qy	1441	GGAGCCGGTAACTGCTCTGCTCGCTCATATATGCACTTCCTTTTAACATGCGAAGAAAT	1500
Db	1471	GGAGCCGGTAACTGCTCTGCTCGCTCATATATGCACTTCCTTTTAACATGCGAAGAAAT	1530
Qy	1501	TTTTAAATATAATTTTATTAAT	1522
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1522	100.0	1522	2	US-08-477-504A-1 Sequence 1, Appl1
3	1522	100.0	1522	2	US-08-486-756A-1 Sequence 1, Appl1
4	1522	100.0	1522	2	US-08-485-862B-1 Sequence 1, Appl1
5	1522	100.0	1522	3	US-08-787-739-1 Sequence 1, Appl1
6	1522	100.0	1522	3	US-08-487-077A-1 Sequence 1, Appl1
7	1522	100.0	1522	3	US-08-485-863A-1 Sequence 1, Appl1
8	1522	100.0	1522	3	US-08-485-049D-1 Sequence 1, Appl1
9	1522	100.0	1522	3	US-09-178-115-1 Sequence 1, Appl1
10	1522	100.0	1522	3	US-09-177-776-1 Sequence 1, Appl1
11	1522	100.0	1522	4	US-09-772-719B-1 Sequence 1, Appl1
12	1522	100.0	1522	4	US-08-260-190-5 Sequence 5, Appl1
13	1416.8	93.1	5052	4	US-08-260-190-23 Sequence 23, Appl1
14	1399	91.9	1399	4	US-08-335-469-1 Sequence 1, Appl1
15	1399	91.9	1399	4	US-08-260-190-1 Sequence 1, Appl1
16	1302.8	85.6	1397	1	US-07-964-589-1 Sequence 1, Appl1
17	1302.8	85.6	1397	1	US-07-964-589-1 Sequence 1, Appl1
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22	10898	27.2	10898	2	US-08-485-862B-5 Sequence 5, Appl1
23	10898	27.2	10898	3	US-08-787-739-5 Sequence 5, Appl1
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32	413.4	27.2	415	2	US-08-485-862B-28 Sequence 28, Appl1
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36	413.4	27.2	445	3	US-08-787-739-28 Sequence 28, Appl1
37	413.4	27.2	445	3	US-09-178-115-28 Sequence 28, Appl1
38	413.4	27.2	445	3	US-09-177-776-28 Sequence 28, Appl1
39	413.4	27.2	445	4	US-09-772-719B-28 Sequence 28, Appl1
40	233.4	15.3	470	2	US-08-481-658B-55 Sequence 55, Appl1
41	233.4	15.3	470	2	US-08-477-504A-55 Sequence 55, Appl1
42	233.4	15.3	470	2	US-08-486-756A-55 Sequence 55, Appl1
43	233.4	15.3	470	2	US-08-485-862B-55 Sequence 55, Appl1
44	233.4	15.3	470	3	US-08-787-739-55 Sequence 55, Appl1
45	233.4	15.3	470	3	US-08-487-077A-55 Sequence 55, Appl1

ALIGNMENTS

RESULT 1
US-08-481-658B-1
; Sequence 1, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-481-658B-1
Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	ACACTGACGGCAATGAGTCTCCCTGTGCGCCAGCCGCCCTGGCTCCCTGTGTATATCCCGGCC	60
Db	1 ACACTGACGGCAATGAGTCTCCCTGTGCGCCAGCCGCCCTGGCTCCCTGTGTATATCCCGGCC	60
Qy	CTGTCTCAAGGCTCATCTGTGCATCTGTGTCTCATCTGTCTTCTGTAGTCTGTCCAT	120
Db	61 CTGTCTCAAGGCTCATCTGTGCATCTGTGTCTCATCTGTCTTCTGTAGTCTGTCCAT	120
Qy	CCCCAGAGATTGCCCGGSAATGCAAGAGAAATCCCCCTTGGGAGAGAGCTTTCTTGGGAA	180
Db	121 CCCCAGAGATTGCCCGGSAATGCAAGAGAAATCCCCCTTGGGAGAGAGCTTTCTTGGGAA	180
Qy	181 GATGACCCACTGGGCGAGAGAGATCTGTCCCATGTGAAGAAGATTCAACCCAGAGAGAGAT	240
Db	181 GATGACCCACTGGGCGAGAGAGATCTGTCCCATGTGAAGAAGATTCAACCCAGAGAGAGAT	240
Qy	241 CCACCCCGAGAGAGAGATCTACTGTGAAGAGAGATCTACTGTGAAGAGAGATCTA	300
Db	241 CCACCCCGAGAGAGAGATCTACTGTGAAGAGAGATCTACTGTGAAGAGAGATCTA	300
Qy	301 GAATTTAAGCTTAATCAGAAAGAGAGGAGTCCCTGAAGTTAGAGAGATCTACCTA	360
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Qy	361 GAGGCTCTTGAGATCTCAGAAACCCAGAAATAATGCCACAGAGGACAAAGAGAGGAT	420
Db	361 GAGGCTCTTGAGATCTCAGAAACCCAGAAATAATGCCACAGAGGACAAAGAGAGGAT	420
Qy	421 GACCAAGATATTGGGCTATGAGAGGCGACCGGCTGTGGCCCGGGATCTCCCAAGCTTC	480
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Qy	481 GCGGCGCGCTTCCAGTCCCGGATGATATCCGCCGCCAGCTGCGGCTTCTGTGCGCGGC	540
Db	481 GCGGCGCGCTTCCAGTCCCGGATGATATCCGCCGCCAGCTGCGGCTTCTGTGCGCGGC	540
Qy	541 CTGTGCCCCCTTGGAACTCTGTGGCTTCCAGTCTCCGCGCTCCAGAACTGTGCGCTGCG	600
Db	541 CTGTGCCCCCTTGGAACTCTGTGGCTTCCAGTCTCCGCGCTCCAGAACTGTGCGCTGCG	600
Qy	601 AACATATGACCAAGTGTGCACTGACCCCTGCTCGGGGCTAGAGATGGCTGTGGATCCC	660
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Qy	661 GGGGCGGAGTACCGGCTCTGTGAGCTGTGCACTGTGGGCGCTGTGAGATGCTGTGCGGGC	720
Db	661 GGGGCGGAGTACCGGCTCTGTGAGCTGTGCACTGTGGGCGCTGTGAGATGCTGTGCGGGC	720
Qy	721 TCGGAGCACTGTGTGAAGGCGACCGTTTCCCTGCGAGATTCACAGTGTTCACCTCAGC	780
Db	721 TCGGAGCACTGTGTGAAGGCGACCGTTTCCCTGCGAGATTCACAGTGTTCACCTCAGC	780
Qy	781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGTGGGCGCCCGGAGAGGCTTGTGCGTGTGGCC	840
Db	781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGTGGGCGCCCGGAGAGGCTTGTGCGTGTGGCC	840
Qy	841 GCTTTTCTGTGAAGAGGGCCCGAAGAAACATGTGCTTATGACAGTTGTCTGTGCTTG	900
Db	841 GCTTTTCTGTGAAGAGGGCCCGAAGAAACATGTGCTTATGACAGTTGTCTGTGCTTG	900
Qy	901 GAAGAAATGCTAGAGAGAGCTCAGAGATCAGAGTCCAGAGACTGTGACATATGTGACATC	960
Db	901 GAAGAAATGCTAGAGAGAGCTCAGAGATCAGAGTCCAGAGACTGTGACATATGTGACATC	960
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QY	1201	AGTCTCTGGGGCTGTGTAGGACGAGTCCAGCTGAAATTCCTGCGCTGTGCTGTGTGAGCATCTTA	1260
Db	1201	AGTCTCTGGGGCTGTGTAGGACGAGTCCAGCTGAAATTCCTGCGCTGTGCTGTGTGAGCATCTTA	1260
QY	1261	GCCTCTGGTTTTTGCGCTCTCTTTTGTCTGTGACCAAGCTGCGTTCCTTTGTGAGATGAGA	1320
Db	1261	GCCTCTGGTTTTTGCGCTCTCTTTTGTCTGTGACCAAGCTGCGTTCCTTTGTGAGATGAGA	1320
QY	1321	AGGCGACACAGAAAGGGGAAACCAAGGGGGGTGTAGCTACCGGCCACGACAGGTAGCCGAG	1380
Db	1321	AGGCGACACAGAAAGGGGAAACCAAGGGGGGTGTAGCTACCGGCCACGACAGGTAGCCGAG	1380
QY	1381	ACTGAGACCTTAGAGGCGCTGATCTTGGAGATGTGAGAAAGCAGCCAGACGACATCTGAGGG	1440
Db	1381	ACTGAGACCTTAGAGGCGCTGATCTTGGAGATGTGAGAAAGCAGCCAGACGACATCTGAGGG	1440
QY	1441	GGAGCCGGTAACTGTCTGTCTTGTCTCATTTATGCCATTCCTTTTAACTGCCAAGAAATT	1500
Db	1441	GGAGCCGGTAACTGTCTGTCTTGTCTCATTTATGCCATTCCTTTTAACTGCCAAGAAATT	1500
QY	1501	TTTTTAAATTAATATTTTAAAT	1522
Db	1501	TTTTTAAATTAATATTTTAAAT	1522

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1      RESULT 2
2      US-08-477-504A-1
3      Sequence 1, Application US/08477504A
4      Patent No. 597235
5      GENERAL INFORMATION:
6      APPLICANT: Zavada, Jan
7      APPLICANT: Pastorekova, Silvia
8      APPLICANT: Pastorek, Jaromir
9      TITLE OF INVENTION: "N Gene and Protein
10     NUMBER OF SEQUENCES: 86
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Leona L. Lauder
13     STREET: 6 Mariposa Court
14     CITY: Tiburon
15     STATE: California
16     COUNTRY: USA
17     ZIP: 94920
18
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/477,504A
26     FILING DATE: 07-JUN-1995
27     CLASSIFICATION: 424
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 08/260,190
30     FILING DATE: 15-JUN-1994
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Lauder, Leona L.
33     REGISTRATION NUMBER: 30,863
34     REFERENCE/DOCKET NUMBER: D-0021.3D
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: 415-435-2034
37     TELEFAX: 415-435-0727
38     INFORMATION FOR SEQ ID NO: 1:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 1522 base pairs
41     TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-477-504A-1

Query Match 100.0% Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACAGTCAAGCCGATGAGTCTCCCTGTCGCCAGCCCTGCTCTCTGTTGATCCCGGCC 60
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DB 121 CCCAGAGGTTGCCCCGAGTGAAGAGATTCCTCTGGAGAGAGGCTCTTCTGGAGAA 180
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DB 481 GGGGGCCGCTTCCAGTCCCGGCTGAATCCCGCCCACTGCGCGCTTCTGCGCGGCC 540
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DB 721 TCGAGACACACTGTGAGAGAGCCAGTTCCTGCGAGATTCACCTGTTCACTCAAC 780
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DB 781 ACCGCTTTTCCAGAGTTGACAGAGGCTTGGGGGCGCGGAGAGGCTGCGCGTGGTGC 840
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DB 1501 TTTTAAATTAATTTTAAAT 1522
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RESULT 3
US-08-486-756A-1
Sequence 1, Application US/08486756A
Patent No. 5981711
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,756A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: lauder, leona l.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCAATGCTCCCTGTCGCCCCAGCCCTGAGCTCTCTGTGATCCCGGCC 60
DB 1 ACAGTCAGCCGCAATGCTCCCTGTCGCCCCAGCCCTGAGCTCTCTGTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 CCCGAGAGGTTGCCCCGAGTGAAGAGATTTCCCTTGGAGAGAGCTCTTCTGGAGAA 180
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DB 481 GCGGAGCCGCTTCACTGCTCCGAGTGAATTCGCGCCCAAGCTGCGCTTCTGCGCGCC 540
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DB 601 AACATGAGCAAGTGTGCACTGACCTGCTCTGAGGCTAAGAGATGAGCTTGGGTCCC 660
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DB 661 GGGCGGAGATCCGGGCTCTGAGCTGATCTGCACTGAGGAGCTGCAAGTCTGCGGCC 720
QY 721 TCGAGGACACTGTGAGAGGCGACCGTTTCCCTGCGAGATTCAGTGTTCCTACCTAGC 780
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QY 781 ACCGCTTTGCCAGATTGACGAGGCTTTGGGGCGCCCGGAGAGGCTGAGCTGTGGCC 840
DB 781 ACCGCTTTGCCAGATTGACGAGGCTTTGGGGCGCCCGGAGAGGCTGAGCTGTGGCC 840
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DB 841 GCGCTTCTGAGAGAGGCGCGGAGAGAAAGTGTCTATGAGCACTGCTGCTGCTGCTG 900
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RESULT 4
US-08-485-862B-1
Sequence 1, Application US/08485862B
Patent No. 598938
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MY Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-862B-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTACAGCGGATGCTCCCTGTCGCCAAGCCCTGCTCTGTTGATCCGGCC 60
DB 1 AAGTACAGCGGATGCTCCCTGTCGCCAAGCCCTGCTCTGTTGATCCGGCC 60
QY 61 CCGTCCAGGCGCTCACTGTCGAACGCTGCTGCTCACTGCTGCTGATGCTGCT 120
DB 61 CCGTCCAGGCGCTCACTGTCGAACGCTGCTGCTCACTGCTGCTGATGCTGCT 120
QY 121 CCCAGAGGTTGCCCCGATGAGAGATTCCCCCTGGAGAGAGCTTTCTGGGAA 180
DB 121 CCCAGAGGTTGCCCCGATGAGAGATTCCCCCTGGAGAGAGCTTTCTGGGAA 180
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DB 181 GATGACCCACTGGGCGAGAGGATCTGCCAATGAAGAGATTCAACCAGAGAGAGAT 240
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DB 241 CCAACCGGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTA 300
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DB 301 GAAGTTAAGCTAAATCAGAAGAGAGGCTCCCTGAAGTTAGAGATCTACTACT 360
QY 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAAGCCACAGGAGCAAAAGAGGAGAT 420
DB 361 GAGGCTCTGAGAGATCTCAAGAACCCAGAAATTAAGCCACAGGAGCAAAAGAGGAGAT 420
QY 421 GACCAAGATCATTTGGGCTATGAGAGGCGACCGGCTGAGCCCGGGTGTCCCAAGCTAC 480
DB 421 GACCAAGATCATTTGGGCTATGAGAGGCGACCGGCTGAGCCCGGGTGTCCCAAGCTAC 480
QY 481 GCGGCGCGCTTCAAGTCCCGGCTGATATCCGCGCCCACTGCGCGCTTCTGCGCGCC 540
DB 481 GCGGCGCGCTTCAAGTCCCGGCTGATATCCGCGCCCACTGCGCGCTTCTGCGCGCC 540
QY 541 CTGCGCGCGCTTCAAGTCCCGGCTTCTGAGCTCCGCGCGCTTCTGAGAGCTGCGCGCC 600
DB 541 CTGCGCGCGCTTCAAGTCCCGGCTTCTGAGCTCCGCGCGCTTCTGAGAGCTGCGCGCC 600

QY 601 AACAAATGCGCAGATGTCAGTCACTGCTCCTGCGCTAGAGATGCTGCGCTCC 660
DB 601 AACAAATGCGCAGATGTCAGTCACTGCTCCTGCGCTAGAGATGCTGCGCTCC 660
QY 661 GGGCGGAGTACCGGGCTTCTGAGCTGATCTGCACTGGGGGCTGAGTCTCCGGCC 720
DB 661 GGGCGGAGTACCGGGCTTCTGAGCTGATCTGCACTGGGGGCTGAGTCTCCGGCC 720
QY 721 TGGGAGCACTGTGGAAGGCGACCGGTTCCCGGCGAGATCAAGTGTTCACCTCAG 780
DB 721 TGGGAGCACTGTGGAAGGCGACCGGTTCCCGGCGAGATCAAGTGTTCACCTCAG 780
QY 781 ACCGCTTTCAGAGATTGACAGAGGCTTGGGCGCGCCGAGAGGCTGCGCTGTGCGC 840
DB 781 ACCGCTTTCAGAGATTGACAGAGGCTTGGGCGCGCGCCGAGAGGCTGCGCTGTGCGC 840
QY 841 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGCATGCTGTCTGCTTG 900
DB 841 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGCATGCTGTCTGCTTG 900
QY 901 GAAGAAATGCTGAGAGAGGCTCAAGACTCAGTCCAGGACTGAGCATATCTGACATC 960
DB 901 GAAGAAATGCTGAGAGAGGCTCAAGACTCAGTCCAGGACTGAGCATATCTGACATC 960
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DB 961 CTGCGCTTCACTTCAAGCGCTACTTCAATATGAGGCTCTCTGACTACACCGCCCTGT 1020
QY 1021 GCCCAGGCTGATCTGATGATGCTGTTTAAACAGACAGTATGCTGATGCTAAGCATC 1080
DB 1021 GCCCAGGCTGATCTGATGATGCTGTTTAAACAGACAGTATGCTGATGCTAAGCATC 1080
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DB 1321 AGGACGACAGAGAGGAGACCAAGGGGCTGAGCTACCGCCAGAGAGTGAAGCCGAG 1380
QY 1381 ACTGAGCTTGAAGGCTGATCTTGAAGATGTGAAGCCAGCCAGAGGATCTGAGGG 1440
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QY 1441 GGAAGCGGTAATCTGCTCTCTGCTCATTAAGCCCTCTTTAACTGCCAAGAAAT 1500
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QY 1501 TTTTAAATTAATTAATTAAT 1522
DB 1501 TTTTAAATTAATTAATTAAT 1522

RESULT 5
US-08-787-739-1
Sequence 1, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-787-739-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGGATGCTCCCTGTGCCCCAGCCCTGTGCTCCCTGTGATCCCGGCC 60
DB 1 AACAGTCAGCGGATGCTCCCTGTGCCCCAGCCCTGTGCTCCCTGTGATCCCGGCC 60
QY 61 CTTGCTCCAGGCTCACTGTGCACTGCTGTGCACTGCTGTGCTGTGATGCTGTGCAT 120
DB 61 CTTGCTCCAGGCTCACTGTGCACTGCTGTGCACTGCTGTGCTGTGATGCTGTGCAT 120
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DB 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCAACCAAGAGAGAGAT 240
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DB 601 AACATGCGCAAGTGTGCACTGACCTGCTCTGCGCTGAGAGATGCTCTGCGGTCC 660
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DB 661 GGGGCGGAGTACCGGCTCTGCACTGATGTGCACTGCGGGGGCTGCAAGTCTCGCGGC 720
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DB 721 TCGGAGCACTGTGGAAGGCGACCGTTTCCCTGCGAGATCAAGTGTCACTGACG 780
QY 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGGCGCCGAGAGGCTGCGCGGTGCGC 840
DB 781 ACCGCTTTGCGAGAGTTGACGAGGCTTGGGGGCGCCGAGAGGCTGCGCGGTGCGC 840
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DB 841 GCGTTTCTGAGAGAGGCGCCGAGAGAAACAGTCCATATGACAGTGTCTGCGCTTG 900
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DB 901 GAAGAAATCGCTGAGAGAGGCTCAGAGACTCAGGTTCCAGAGCTGACATATGCACTC 960
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DB 1021 GCCCAGGGTGCATCTGAGCTGTGTAAACAGACAGTATGCTGATGCTAAACAGCTC 1080
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DB 1081 CACACCTCTCTGACACCTGTGGGAGCTGTGATCTCGGGCTACAGCTGAACCTTCCGA 1140
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DB 1141 GCGAGCGAGGCTTTGAATGAGCGAGATGATGAGGCTCTTCCCTGCTGAGTGAAGC 1200
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Db 1261 GCCCTGTTTGGCTCTCTTTTGTCTACACAGCGCTGCGTTCCTTGAGAGATAGA 1320
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 Db 1322 AGGACGACAGAGGGGAGCAAGGGGGTGTGAGTACGGCCAGAGAGGAGCCGAG 1380
 QY 1381 ACTGAGCTTAGAGGCTGATCTTGGAGATGTGAGAGCCAGCCAGAGCACTTGAGGG 1440
 Db 1381 ACTGAGCTTAGAGGCTGATCTTGGAGATGTGAGAGCCAGCCAGAGCACTTGAGGG 1440
 QY 1441 GGAGCCGGTAACTGCTCTGCTGCTCATTTATGCCATCTTTTAACTGCCAAGAAAT 1500
 Db 1441 GGAGCCGGTAACTGCTCTGCTGCTCATTTATGCCATCTTTTAACTGCCAAGAAAT 1500
 QY 1501 TTTTAAATTAATTTATTAAT 1522
 Db 1501 TTTTAAATTAATTTATTAAT 1522

RESULT 6

US-08-487-077A-1
 / Sequence 1, Application US/08487077A
 / Patent No. 6069242
 / GENERAL INFORMATION:
 / APPLICANT: Zavada, Jan
 / APPLICANT: Pastorekova, Silvia
 / APPLICANT: Pastorek, Jaromir
 / TITLE OF INVENTION: MN Gene and Protein
 / NUMBER OF SEQUENCES: 86
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Leona L. Lauder
 / STREET: 6 Mariposa Court
 / CITY: Tiburon
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94920
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/487,077A
 / FILING DATE: 07-JUN-1995
 / CLASSIFICATION: 514
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/260,190
 / FILING DATE: 15-JUN-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Lauder, Leona L.
 / REGISTRATION NUMBER: 30,863
 / REFERENCE/DOCKET NUMBER: D-0021.3H
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-435-2034
 / TELEFAX: 415-435-0727
 / INFORMATION FOR SEQ. ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1522 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / ANTI-SENSE: NO
 / US-08-487-077A-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACAGTCAGCCGATGCTCCCTGTGACCCAGCCCTGCTCCTCTGTGATCCCGGCC 60
 Db 1 ACAGTCAGCCGATGCTCCCTGTGACCCAGCCCTGCTCCTCTGTGATCCCGGCC 60

QY 61 CCTGCTCAGGCTCACTGTGCAACTGTGCTCACTGCTGCTTCTGATGCTGTCAT 120
 Db 61 CCTGCTCAGGCTCACTGTGCAACTGTGCTCACTGCTGCTTCTGATGCTGTCAT 120
 QY 121 CCCAAGAGTTTCCCGAGTGCAGAGAGATTCCTTTGGAGAGAGCTCTTCTGGGAA 180
 Db 121 CCCAAGAGTTTCCCGAGTGCAGAGAGATTCCTTTGGAGAGAGCTCTTCTGGGAA 180
 QY 181 GATGACCCATGGGCGAGAGAGATTCGCGCAATGAAAGAGATTCACCCAGAGAGAGAT 240
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 Db 241 CCACCCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCT 300
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 QY 361 GAGGCTCTGAGATCTTCAAGAACCCAGATTAATGCCACAGAGAGAGAGAGAT 420
 Db 361 GAGGCTCTGAGATCTTCAAGAACCCAGATTAATGCCACAGAGAGAGAGAGAT 420
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 QY 541 CTGCGCCCTTGGAACTCTGAGGCTTCCAGCTTCCGCGCTCCAGAACTGCGGCTGCGC 600
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 QY 601 AACAAATGACAGATGTGCACTGACCCGCTCCGCTGAGATGAGATCTGAGTCC 660
 Db 601 AACAAATGACAGATGTGCACTGACCCGCTCCGCTGAGATGAGATCTGAGTCC 660
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 Db 721 TCGAGACACATGTGAGAGGCCACCGTTTCCCTGCCAGATCCAGTGGTTCACTCAGC 780
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 Db 781 ACCGCTTTGCAAGATTGACAGAGGCTTGGGGGCGCGGAGAGGCTGACCGGTTGGGC 840
 QY 841 GCTTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGACAGTGTCTGCTGCTTGG 900
 Db 841 GCTTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGACAGTGTCTGCTGCTTGG 900
 QY 901 GAAAGAAATGCTGAGAGAGGCTCAAGACTCAAGTTCACAGACTGACATATCTGACATC 960
 Db 901 GAAAGAAATGCTGAGAGAGGCTCAAGACTCAAGTTCACAGACTGACATATCTGACATC 960
 QY 961 CTGCGCTGACCTTCAAGCGGCTCACTTCCAAATGAGGGGTCTCTGACTACACCGCCCTGT 1020
 Db 961 CTGCGCTGACCTTCAAGCGGCTCACTTCCAAATGAGGGGTCTCTGACTACACCGCCCTGT 1020
 QY 1021 GCCCAGAGTGTATCTGACTGTGTTAACAGACAGTATCTGAGTCTAAGAGAGCTC 1080
 Db 1021 GCCCAGAGTGTATCTGACTGTGTTAACAGACAGTATCTGAGTCTAAGAGAGCTC 1080
 QY 1081 CACACCTCTTGAACACCTGTGGGAGCCTGTGATCTCTGCGCTACAGCTGAATCTCCGA 1140
 Db 1081 CACACCTCTTGAACACCTGTGGGAGCCTGTGATCTCTGCGCTACAGCTGAATCTCCGA 1140

Db 961 CTGCCCCCTGACCTTCAAGCCGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
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Db 1141 GCGAGCGACCCCTTTGAATGAGGCGAGTGAATGAGGCTCTCTCTGCTGAGTGAACAC 1200
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QY 1261 GCCCTGCTTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
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QY 1441 GGAGCGGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
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RESULT 8
US-08-485-049D-1
; Sequence 1, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,049D
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-485-049D-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAAGCCGATGAGCTCCCTGTGCTCCAGCCCTGAGCTCCCTGTGATCCCGGCC 60
Db 1 ACAGTCAAGCCGATGAGCTCCCTGTGCTCCAGCCCTGAGCTCCCTGTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCTCTCACTGTGCACTGTCTGTCACTGTCTGTCTGTGATGCTGTCCAT 120
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QY 481 GGGGGCGGCTTCAAGTCCCGGCTGATATCCGCCCCCAGCTGCGGCTTTCGCCGGCC 540
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QY 541 CTGCGCCCTGGAATCTCTGAGGCTTTCAGCTCCGCGCGCTCCAGAACTGAGGCTGCGC 600
Db 541 CTGCGCCCTGGAATCTCTGAGGCTTTCAGCTCCGCGCGCTCCAGAACTGAGGCTGCGC 600
QY 601 AACAAATGCGCAAGTGTGCACTGACCTGCTCTGAGGCTGAGAGTGTGCTGAGGCTCC 660
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Db 781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGGGGCGCCGAGAGGCTGAGGCTGAGGCTGAGC 840

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D	661	GGGGGGGGAGTACCGGGAGCTCTGCAAGCTGCAATCTGCACTGGGGGGGGCTCAGGTCGTCCGGGC	720
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Q	781	ACCGGCTTTGGCCAGATTGACAGAGGCTTTGGGGCGCCCGGAGGCGCTGGCCGTGTGGCC	840
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Q	901	GAGAAATTCGCTGAGGAAAGGCTCAGAGACTCAGGTCCAGAACTGGACATATCTGACATC	960
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Q	1021	GCCGAGGGGTATCTGGACTGTGTTTAAACAGACAGTGAATGCTAGATGCTAAGCAGCTC	1080
D	1021	GCCGAGGGGTATCTGGACTGTGTTTAAACAGACAGTGAATGCTAGATGCTAAGCAGCTC	1080
Q	1081	CACACCTCTCTGACACCCCTGTGGGGACCTGTGACTCTCGGCTACAGCTGAATCTCCGA	1140
D	1081	CACACCTCTCTGACACCCCTGTGGGGACCTGTGACTCTCGGCTACAGCTGAATCTCCGA	1140
Q	1141	GCGACGACAGCCTTTGAAATGGGCGAGATTTGAGGCGCTCTTCTCGTGGAGTGAACAGC	1200
D	1141	GCGACGACAGCCTTTGAAATGGGCGAGATTTGAGGCGCTCTTCTCGTGGAGTGAACAGC	1200
Q	1201	AGTCTCGGGCGTGAAGCCACATCCAGCTGAATTCCTGCGTGGCTGTGTGACATCCTA	1260
D	1201	AGTCTCGGGCGTGAAGCCACATCCAGCTGAATTCCTGCGTGGCTGTGTGACATCCTA	1260
Q	1261	GCCCTGTATTTTGGGCTCTTTTGGCTGCACACAGGTGGCTTCTGTGCAAGATGAGA	1320
D	1261	GCCCTGTATTTTGGGCTCTTTTGGCTGCACACAGGTGGCTTCTGTGCAAGATGAGA	1320
Q	1321	AGGCAACACAGAAAGGGAAACAAAGGGGGGTGTGACTTACCGCCACAGAGATGACCGAG	1380
D	1321	AGGCAACACAGAAAGGGAAACAAAGGGGGGTGTGACTTACCGCCACAGAGATGACCGAG	1380
Q	1381	ACTGAGGCTTAAAGGCTGGAATCTTGGAGAAATGTGAAGCCAGCCAGAGGCATCTAGGG	1440
D	1381	ACTGAGGCTTAAAGGCTGGAATCTTGGAGAAATGTGAAGCCAGCCAGAGGCATCTAGGG	1440
Q	1441	GGAGCCGGTAACTGTCTGTCTCTGCTCATTTATGACACTTCTTTTAACTGCCAAGAAAT	1500
D	1441	GGAGCCGGTAACTGTCTGTCTCTGCTCATTTATGACACTTCTTTTAACTGCCAAGAAAT	1500
Q	1501	TTTTTAAATTAATATTTATTAAT	1520
D	1501	TTTTTAAATTAATATTTATTAAT	1520

RESULT 10
 US-09-177-776-1
 Sequence 1, Application US/09177776A
 Patent No. 6297051
 GENERAL INFORMATION:
 APPLICANT: Zavada, Jan
 APPLICANT: Pastorekova, Silvia
 APPLICANT: Pastorek, Jaromir
 TITLE OF INVENTION: NM Gene and Protein

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1 FILE REFERENCE: D-0021.5A
2
3 CURRENT APPLICATION NUMBER: US/09/177,776A
4
5 CURRENT FILING DATE: 1998-10-23
6
7 EARLIER APPLICATION NUMBER: 08/787,739
8
9 EARLIER FILING DATE: 1997-01-24
10
11 EARLIER APPLICATION NUMBER: 08/485,049
12
13 EARLIER FILING DATE: 1995-06-07
14
15 EARLIER APPLICATION NUMBER: 08/486,756
16
17 EARLIER FILING DATE: 1995-06-07
18
19 EARLIER APPLICATION NUMBER: 08/477,504
20
21 EARLIER FILING DATE: 1995-06-07
22
23 EARLIER APPLICATION NUMBER: 08/481,658
24
25 EARLIER FILING DATE: 1995-06-07
26
27 EARLIER APPLICATION NUMBER: 08/485,862
28
29 EARLIER FILING DATE: 1995-06-07
30
31 EARLIER APPLICATION NUMBER: 08/485,863
32
33 EARLIER FILING DATE: 1995-06-07
34
35 EARLIER APPLICATION NUMBER: 08/487,077
36
37 EARLIER FILING DATE: 1995-06-07
38
39 EARLIER APPLICATION NUMBER: 08/260,190
40
41 EARLIER FILING DATE: 1994-06-15
42
43 EARLIER APPLICATION NUMBER: 08/177,093
44
45 EARLIER FILING DATE: 1993-12-30
46
47 EARLIER APPLICATION NUMBER: 07/964,589
48
49 EARLIER FILING DATE: 1992-10-21
50
51 EARLIER APPLICATION NUMBER: PV-709-92
52
53 EARLIER FILING DATE: 1992-03-11
54
55 NUMBER OF SEQ ID NOS: 116
56
57 SOFTWARE: PatentIn Ver. 2.0
58
59 SEQ ID NO 1
60
61 LENGTH: 1522
62
63 TYPE: DNA
64
65 ORGANISM: HUMAN
66
67 FEATURE:
68
69 NAME/KEY: CDS
70
71 LOCATION: (13)..(1389)
72
73 FEATURE:
74
75 NAME/KEY: mat_peptide
76
77 LOCATION: (124)..(1389)
78
79 US-09-177-776-1

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Query Match	100.0%	Score 1522	DB 3	Length 1522
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1522	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ACAGTCACCGCATGCTCCCTGTGCCCCACCGCCTGGCTCCCTGTGTTATCCGGCC	60	
Db	1	ACAGTCACCGCATGCTCCCTGTGCCCCACCGCCTGGCTCCCTGTGTTATCCGGCC	60	
QY	61	CCTGCTCAGGCTTCATCTGTGCAACTGTGTGTTCATCTGCTGCTTTTGATGCCCTGTCCAT	120	
Db	61	CCTGCTCAGGCTTCATCTGTGCAACTGTGTGTTCATCTGCTGCTTTTGATGCCCTGTCCAT	120	
QY	121	CCCCAGAGGTTCGCCCGATGCAAGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGAA	180	
Db	121	CCCCAGAGGTTCGCCCGATGCAAGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGAA	180	
QY	181	GATGATCCCATCTGGCGAGAGATCTGCCCATGTAAAGAGATTCACCAGAGAGAGAT	240	
Db	181	GATGATCCCATCTGGCGAGAGATCTGCCCATGTAAAGAGATTCACCAGAGAGAGAT	240	
QY	241	CCACCCGGAGAGAGATCTACCTGTGAGAGAGATCTACCTGTGAGAGAGATCTACCT	300	
Db	241	CCACCCGGAGAGAGATCTACCTGTGAGAGAGATCTACCTGTGAGAGAGATCTACCT	300	
QY	301	GAAGTTAAGCTTAATCAGAGAAAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGTT	360	
Db	301	GAAGTTAAGCTTAATCAGAGAAAGAGGCTCCCTGAAGTTAGAGATCTACCTACTGTT	360	
QY	361	GAGGCTCTGGAGATCTCTCAAGAAACCCAGATTAATGCCCAAGAGCAAAAGAGGGAT	420	
Db	361	GAGGCTCTGGAGATCTCTCAAGAAACCCAGATTAATGCCCAAGAGCAAAAGAGGGAT	420	

D	b		241	CCACCCGGAGAGAGATCTACCTGAGAGAGATCTACTGAGAGAGATCTACT	300
O	y		301	GAAGTTAAGCTTAATCAGAAGAAAGGCCTCCCTGAAGTTAAGAGATCTACTGTT	360
D	b		301	GAAGTTAAGCTTAATCAGAAGAAAGAGGCCTCCCTGAAGTTAAGAGATCTACTGTT	360
O	y		361	GAGGCTCTTGAGATTCCTCAAGAACCCCGAATAATGCCCAAGAGACAAGAAAGGGAT	420
D	b		361	GAGGCTCTTGAGATTCCTCAAGAACCCCGAATAATGCCCAAGAGACAAGAAAGGGAT	420
O	y		421	GACCAGAGTCAATTGGCGCTATGAGAGCAGCCCGCCTGGCCCCGGAGTGTCCCAGCCTGC	480
D	b		421	GACCAGAGTCAATTGGCGCTATGAGAGCAGCCCGCCTGGCCCCGGAGTGTCCCAGCCTGC	480
O	y		481	GCGGGCGGCTTCCAGTCCCGGATGATATCCGCCCCAGCTCGCGGCTTGTGCGCGGC	540
D	b		481	GCGGGCGGCTTCCAGTCCCGGATGATATCCGCCCCAGCTCGCGGCTTGTGCGCGGC	540
O	y		541	CTGGGCCCCCTGGAATCTCTGGGCTTCAAGCTCCGCGCTCCAGAACTGCGCTGCGC	600
D	b		541	CTGGGCCCCCTGGAATCTCTGGGCTTCAAGCTCCGCGCTCCAGAACTGCGCTGCGC	600
O	y		601	AACAATGGSCACAGTGTCAA CTGACCCGTGCTCCCTGGCTTAGAGATGGCTCTGGATCC	660
D	b		601	AACAATGGSCACAGTGTCAA CTGACCCGTGCTCCCTGGCTTAGAGATGGCTCTGGATCC	660
O	y		661	GGGCGGAGTACCGGGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTCTGCCGGC	720
D	b		661	GGGCGGAGTACCGGGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTCTGCCGGC	720
O	y		721	TGGAAGCACACTGTGGAAAGGCCACCGTTCCTGTCCGTGAGATCCAGTGTCACTCAAGC	780
D	b		721	TGGAAGCACACTGTGGAAAGGCCACCGTTCCTGTCCGTGAGATCCAGTGTCACTCAAGC	780
O	y		781	ACCGGCTTTCAGAGTTAGAGAGGCCCTTGGGGGGCCCGGAGGCTGGCGGTGTGGCC	840
D	b		781	ACCGGCTTTCAGAGTTAGAGAGGCCCTTGGGGGGCCCGGAGGCTGGCGGTGTGGCC	840
O	y		841	GCTTTCCTGAGAGAGGGCCCGGAAAGAAAACAAGTGCCTATGAGCAATTGCTCTCGCTTG	900
D	b		841	GCTTTCCTGAGAGAGGGCCCGGAAAGAAAACAAGTGCCTATGAGCAATTGCTCTCGCTTG	900
O	y		901	GAAAGAAATCGTGAAGAAAGGCTCAGAGACTCAAGTCCAGAGACTGGAATATCTGCACTC	960
D	b		901	GAAAGAAATCGTGAAGAAAGGCTCAGAGACTCAAGTCCAGAGACTGGAATATCTGCACTC	960
O	y		961	CTGCGCTTGAATTCAGCGGCTACTTCCAAATATGAGGGGTCTTGACCTAACCCGCTGT	1020
D	b		961	CTGCGCTTGAATTCAGCGGCTACTTCCAAATATGAGGGGTCTTGACCTAACCCGCTGT	1020
O	y		1021	GCCGAGGGTGCATCTGGAATGTGTITTAACAGACAGATGATGATGCTTAAGCAGCTC	1080
D	b		1021	GCCGAGGGTGCATCTGGAATGTGTITTAACAGACAGATGATGATGCTTAAGCAGCTC	1080
O	y		1081	CACAACCTCTCTGACACCCCTGTGGGAACCTGTGATCTCTCGGCTAACACTGAATCTTCGA	1140
D	b		1081	CACAACCTCTCTGACACCCCTGTGGGAACCTGTGATCTCTCGGCTAACACTGAATCTTCGA	1140
O	y		1141	GCAGACGACGCTTTGAATGGGGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGGACAGC	1200
D	b		1141	GCAGACGACGCTTTGAATGGGGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGGACAGC	1200
O	y		1201	AGTCTCGGGGCTGAGACAGTCCAGCGTAATTCCTGCGCTGAGTGGACATCTCTTA	1260
D	b		1201	AGTCTCGGGGCTGAGACAGTCCAGCGTAATTCCTGCGCTGAGTGGACATCTCTTA	1260
O	y		1261	GCCCTGTATTTTGGCTCTCTTTTGTCTGACACAGCTCGGATTCCTGTGCAATGAGA	1320
D	b		1261	GCCCTGTATTTTGGCTCTCTTTTGTCTGACACAGCTCGGATTCCTGTGCAATGAGA	1320
O	y		1321	AGGACGACACAGAGGGGAACCAAGGGGGTGTAGCTACCGCCACGACAGGTAGCCGAG	1380
D	b		1321	AGGACGACACAGAGGGGAACCAAGGGGGTGTAGCTACCGCCACGACAGGTAGCCGAG	1380

QY	DB	Sequence	Score	Pred.	Indels	Gaps
QY	1321	AGGAGACACGAAAGGGGAAACCAAGGGGGGTGTGAGCTACCGCCACGACGAGAGTGGCCGAG	1380			
QY	1381	ACTGAGCCCTTAGAGCTGTGATCTTTGAGAAATGTGAAAGCCAGCCAGAGCATGTGAGGG	1440			
DB	1381	ACTGAGCGCTTAGAGGCTGTGANTCTTGGAGAAATGTGAAAGCCAGCGGATCTTGAGGG	1440			
QY	1441	GGAGCCGGTAACTGTCTCTGTCTGCTCATTAATGACACTTCTCTTTAACTGCGAAGAAAT	1500			
DB	1441	GGAGCCGGTAACTGTCTCTGTCTGCTCATTAATGACACTTCTCTTTAACTGCGAAGAAAT	1500			
QY	1501	TTTTAAATAATAATTTATAAT	1522			
DB	1501	TTTTAAATAATAATTTATAAT	1522			
<p>RESULT 12</p> <p>US-08-260-190-5</p> <p>; Sequence 5, Application US/08260190A</p> <p>; Patent No. 6774117</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Zavada, Jan</p> <p>; APPLICANT: Pastorekova, Silvia</p> <p>; APPLICANT: Pastorek, Jaromir</p> <p>; TITLE OF INVENTION: MN Gene and Protein</p> <p>; FILE REFERENCE: D-0021-2</p> <p>; CURRENT APPLICATION NUMBER: US/08/260,190A</p> <p>; CURRENT FILING DATE: 1994-06-15</p> <p>; EARLIER APPLICATION NUMBER: 08/177,093</p> <p>; EARLIER FILING DATE: 1993-12-30</p> <p>; EARLIER APPLICATION NUMBER: 07/964,589</p> <p>; EARLIER FILING DATE: 1992-10-21</p> <p>; EARLIER APPLICATION NUMBER: PV-709-92</p> <p>; EARLIER FILING DATE: 1992-03-11</p> <p>; NUMBER OF SEQ ID NOS: 26</p> <p>; SOFTWARE: PatentIn Ver. 2.0</p> <p>; SEQ ID NO 5</p> <p>; LENGTH: 1522</p> <p>; TYPE: DNA</p> <p>; ORGANISM: HUMAN</p> <p>; FEATURE:</p> <p>; NAME/KEY: CDS</p> <p>; LOCATION: (13)..(1389)</p> <p>; FEATURE:</p> <p>; NAME/KEY: mat_peptide</p> <p>; LOCATION: (124)..(1389)</p> <p>US-08-260-190-5</p>						
<p>Query Match 100.0%; Score 1522; DB 4; Length 1522;</p> <p>Best Local Similarity 100.0%; Pred. No. 0;</p> <p>Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>						
QY	1	ACAGTCAGCCGCATGAGCTCCCTGTGCCCCAGCCCCGTGCTCCTCTGTGATCCCGCC	60			
DB	1	ACAGTCAGCCGCATGAGCTCCCTGTGCCCCAGCCCCGTGCTCCTCTGTGATCCCGCC	60			
QY	61	CTGTCTCAGGCTCTCATCTGTGCAACTGTGCTGTCTCATCTGTCTTGATCCTGTGCTCAT	120			
DB	61	CTGTCTCAGGCTCTCATCTGTGCAACTGTGCTGTCTCATCTGTCTTGATCCTGTGCTCAT	120			
QY	121	CCCCAGAGTTGGCCCCCGGATGACAGAGATTTCCCCCTTGGAGAGAGCTCTTCTGGGGA	180			
DB	121	CCCCAGAGTTGGCCCCCGGATGACAGAGATTTCCCCCTTGGAGAGAGCTCTTCTGGGGA	180			
QY	181	GATGACCCACTGTGGGCGAGAGATCTGCCCCAGTGAAGATTCACCCAGAGAGAGAT	240			
DB	181	GATGACCCACTGTGGGCGAGAGATCTGCCCCAGTGAAGATTCACCCAGAGAGAGAT	240			
QY	241	CAACCCGAGAGAGAGATCTTCACTGTGAGAGAGATCTTCACTGTGAGAGAGAGATCTTCACT	300			
DB	241	CAACCCGAGAGAGAGATCTTCACTGTGAGAGAGATCTTCACTGTGAGAGAGAGATCTTCACT	300			
QY	301	GAGGTAAAGCTTAATCAGAAAGAGGCTCCTGAAAGTTAAGAGATCTTCACTGTT	360			
DB	301	GAGGTAAAGCTTAATCAGAAAGAGGCTCCTGAAAGTTAAGAGATCTTCACTGTT	360			

Db 3961 TCATTGCGCTATGAGGCGACCCG-CCTGGCCCCGGGGTGTCCCAAGCTGCGCGGGCCG 4019
Qy 489 CTTCCAGTCCCGGATATCCGCCCCAGCTGCGCTTTTGGCCCGCCCTTGCGGCC 548
Db 4020 CTTCCAGTCCCGGATATCCGCCCCAGCTGCGCTTTTGGCCCGCCCTTGCGGCC 4079
Qy 549 CTTGGAATCTTGGGCTTCAGACTCCCGCGCTCCAGAACTGCGCTGCGCAACATGG 608
Db 4080 CTTGGAATCTTGGGCTTCAGACTCCCGCGCTCCAGAACTGCGCTGCGCAACATGG 4138
Qy 609 CCAAGTGTGCAATGACCTTCTCTGAGCTAGAGATGGCTCTGAGTCCCGGCGGGA 668
Db 4139 CCAAGTGTGCAATGACCTTCTCTGAGCTAGAGATGGCTCTGAGTCCCGGCGGGA 4198
Qy 669 GTACCGGGCTTCAGCTGATCTGACATGGGGGGCTGACAGTCTCCCGCTCCGAGCA 728
Db 4199 GTACCGGGCTTCAGCTGATCTGACATGGGGGGCTGACAGTCTCCCGCTCCGAGCA 4257
Qy 729 CACTGTGAAAGGCAACCGTTTCCCTGCGAGATCCAGTGTTCACCTGACGCGCTT 788
Db 4258 CACTGTGAAAGGCAACCGTTTCCCTGCGAGATCCAGTGTTCACCTGACGCGCTT 4317
Qy 789 TCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCGGTGGCGCTTCT 848
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Qy 849 GGAAGAGGCGCCGGAAGAAACAGTG-CCTATGAGAGATGTCTCTCTGCTGGAGAA 907
Db 4377 GGAAGAGGCGCCGGAAGAAACAGTG-CCTATGAGAGATGTCTCTCTGCTGGAGAA 4436
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Db 4437 TCGCTGAGAGAGCTCAGAGACTCAGTCCAGAGCTGACATATCTGACCTCTGCT 4496
Qy 968 CTGACTTACCGGCTAATCTCAATATGAGGGGCTCTGACATACCGGCTGTGCCAG 1027
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Qy 1028 GTGTATCTGAGCTGTGTTAAACCAACATGATGTCTGAGTGTAGAGCTTCCACACC 1087
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Qy 1088 TCTCTGACACCGTGTGGGACCTGTGACTCTGGCTACAGCTGAATCCGAGCGACGC 1147
Db 4617 TCTCTGACACCGTGTGGGACCTGTGACTCTGGCTACAGCTGAATCCGAGCGACGC 4676
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Db 4677 AGCTTTGATGAGCGAGTATGAGGCTCTTCTCTGCTGAGTGTGACAGCAGTCTCT 4736
Qy 1208 GGGCTGTGAGCTCAGCTCAGCTGAATCTCTGCTGCTGTGTGACATCTTACCTTGG 1267
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Qy 1328 ACAGAGAGGGAACCAAGGGGGGTGTAGC-TACCGCCAGCAGAGGTAGCCGAGACTGGA 1386
Db 4857 ACAGAGAGGGAACCAAGGGGGGTGTAGC-TACCGCCAGCAGAGGTAGCCGAGACTGGA 4916
Qy 1387 GCTTGAAGGCTGATTTTGAAGATGTGAGAGCCAGGCAAGGCAATCTGAGGGGGAGCC 1446
Db 4917 GCTTGAAGGCTGATTTTGAAGATGTGAGAGCCAGGCAAGGCAATCTGAGGGGGAGCC 4976
Qy 1447 GGTAACTGTCTGTCTGCTCATATGACACTTCTTTTAACTGCGCAAGAAATTTTAA 1506
Db 4977 GGTAACTGTCTGTCTGCTCATATGACACTTCTTTTAACTGCGCAAGAAATTTTAA 5036
Qy 1507 AATAAATATTTAAT 1522
Db 5037 AATAAATATTTAAT 5052

RESULT 14
US-08-335-469-1
; Sequence 1, Application US/08335469A
; Patent No. 6004535
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide
; FILE REFERENCE: D-0021A
; CURRENT APPLICATION NUMBER: US/08/335,469A
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-335-469-1
Query Match 91.9%; Score 1399; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 124 CAGAGTTTCCCCGATGTGAGAGATTTCCCTTGGAGAGAGGCTTCTTGGGAAAGT 183
Db 1 CAGAGTTTCCCCGATGTGAGAGATTTCCCTTGGAGAGAGGCTTCTTGGGAAAGT 60
Qy 184 GACCCACTGGGAGAGAGATGTGCGCCAGTGAAGAGATTCAACCCAGAGAGAGATCCA 243
Db 61 GACCCACTGGGAGAGAGATGTGCGCCAGTGAAGAGATTCAACCCAGAGAGAGATCCA 120
Qy 244 CCGGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGATCTTACCTGAA 303
Db 121 CCGGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAGAGAGATCTTACCTGAA 180
Qy 304 GTTAAAGCTTAATCAGAGAAAGAGGCTTCCCTGAAGTTGAGGATCTTACTGTGAG 363
Db 181 GTTAAAGCTTAATCAGAGAAAGAGGCTTCCCTGAAGTTGAGGATCTTACTGTGAG 240
Qy 364 GCTCCGAGAGATCTCAAGAACCCCAAGATTAATGCCACAGGGAACAAAGGGGATGAC 423
Db 241 GCTCCGAGAGATCTCAAGAACCCCAAGATTAATGCCACAGGGAACAAAGGGGATGAC 300
Qy 424 CAGAGTATTTGCGCTATGAGAGGCAACCGCCCTGAGCCCGGGGTCTCCAGCTTGGCG 483
Db 301 CAGAGTATTTGCGCTATGAGAGGCAACCGCCCTGAGCCCGGGGTCTCCAGCTTGGCG 360
Qy 484 GCGCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGCGCTTCTGCGCGGCTTGG 543
Db 361 GCGCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGCGCTTCTGCGCGGCTTGG 420
Qy 544 GCGCCCCGTGGAATCTCTGGGCTTCAAGCTCCGCGCGCTCCAGAACTGCGGCTGGCAAC 603
Db 421 GCGCCCCGTGGAATCTCTGGGCTTCAAGCTCCGCGCGCTCCAGAACTGCGGCTGGCAAC 480
Qy 604 AATGCGCAAGTGTGCAACTGACCTGTCTCTTGGGCTAGAGATGGCTTGGGCTCCGGG 663
Db 481 AATGCGCAAGTGTGCAACTGACCTGTCTCTTGGGCTAGAGATGGCTTGGGCTCCGGG 540
Qy 664 CCGGAGTACCGGGCTTGTGAGTGTGACATGTGCACTGAGGGGGCTGCAAGTGTCTCGGGCTGG 723
Db 541 CCGGAGTACCGGGCTTGTGAGTGTGACATGTGCACTGAGGGGGCTGCAAGTGTCTCGGGCTGG 600
Qy 724 GAGCACTGTGGAAGGCCACCGTTTCCCTGCGAGATCAAGTGTGTTCACTGACGACCC 783

Db 601 GAGCAGACCTGTGGAGGCAACCGTTCCTGCGAGATCCAGTGTGTTCACTCCAGCACCC 660
Qy 784 GCCTTGGCAGAGTTGACAGAGGCTTGGGCGCCCGGAGAGGCGCTGGCGGTGGCGGCC 843
Db 661 GCCTTGGCAGAGTTGACAGAGGCTTGGGCGCCCGGAGAGGCGCTGGCGGTGGCGGCC 720
Qy 844 TTTCTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGACAGTGTGTTCTGCTGGAGAA 903
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Qy 904 GAAATGCTGAGAGAGGCTCAGAGATCAGAGTCCCGAGCTGAGCAATATCTGACTCTCG 963
Db 781 GAAATGCTGAGAGAGGCTCAGAGATCAGAGTCCCGAGCTGAGCAATATCTGACTCTCG 840
Qy 964 CCTCTGACTGAGCGGCTACTTCCAAATGAGAGGGTCTCTGACTCAGCGCCCTGTGCC 1023
Db 841 CCTCTGACTGAGCGGCTACTTCCAAATGAGAGGGTCTCTGACTCAGCGCCCTGTGCC 900
Qy 1024 CAGGGTGTCTGAGCTGTGTTTAAACAGACAGTATGCTGAGTGTCTAAGCAGCTCCAC 1083
Db 901 CAGGGTGTCTGAGCTGTGTTTAAACAGACAGTATGCTGAGTGTCTAAGCAGCTCCAC 960
Qy 1084 ACCCTCTGAGACCCCTGTGGGAGCCTGTGTGACTCTCGGCTCAGCTGAATCTCCGAGG 1143
Db 961 ACCCTCTGAGACCCCTGTGGGAGCCTGTGTGACTCTCGGCTCAGCTGAATCTCCGAGG 1020
Qy 1144 AGCAGACCTTTGAAATGAGGCGAGTGTGAGGCTCTCTCTGCTGAGTGTGAGCAGCAGT 1203
Db 1021 AGCAGACCTTTGAAATGAGGCGAGTGTGAGGCTCTCTCTGCTGAGTGTGAGCAGCAGT 1080
Qy 1204 CCTCGGCTGTGAGGCTGAGCAGTGTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
Db 1081 CCTCGGCTGTGAGGCTGAGCAGTGTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1264 CTGGTTTTGGCTCTCTTTTGTGCTGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db 1141 CTGGTTTTGGCTCTCTTTTGTGCTGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1324 CAGCAGAGAGGAGAAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACT 1383
Db 1201 CAGCAGAGAGGAGAAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACT 1260
Qy 1384 GAGGCTGTAGAGGCTGTGATTTGAGAGATGTGAGAGCCAGCAGAGGCAATCTGAGGGGGA 1443
Db 1261 GAGGCTGTAGAGGCTGTGATTTGAGAGATGTGAGAGCCAGCAGAGGCAATCTGAGGGGGA 1320
Qy 1444 GCCGGTAACCTGTCTGCTGCTCATTTAGCCACTTCTTTTAACTGCAAGAAATTTT 1503
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Qy 1504 TAAATTAATATTTTAAAT 1522
Db 1381 TAAATTAATATTTTAAAT 1399

RESULT 15
US-08-260-190-1
; Sequence 1, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorek, Sylvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92

; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-260-190-1

Query Match 91.9%; Score 1399; DB 4; Length 1399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 CAGAGTTGGCCCGGAGGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAAAT 183
Db 1 CAGAGTTGGCCCGGAGGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAAAT 60
Qy 184 GACCACTGGGCGAGAGAGATCTGCCAGTGAAGATTCACCCAGAGAGAGATCCA 243
Db 61 GACCACTGGGCGAGAGAGATCTGCCAGTGAAGATTCACCCAGAGAGAGATCCA 120
Qy 244 CCGGAGAGAGATCTTACTGAGAGAGAGATCTTACTGAGAGAGAGATCTTAA 303
Db 121 CCGGAGAGAGATCTTACTGAGAGAGAGATCTTACTGAGAGAGAGATCTTAA 180
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GenCore version 5.1.6
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Run on: February 6, 2005, 03:56:53 ; Search time 860 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1522	100.0	1522	US-09-967-237-1	Sequence 1, Appli
3	1522	100.0	1522	US-10-795-933-5	Sequence 5, Appli
4	1522	100.0	1522	US-10-888-694-1	Sequence 1, Appli
5	1522	100.0	1522	US-09-954-456-89	Sequence 89, Appli
6	1522	100.0	1522	US-09-954-456-726	Sequence 726, App
7	1522	100.0	1522	US-09-960-706-1080	Sequence 1080, Ap
8	1522	100.0	1522	US-09-873-367C-516	Sequence 516, App
9	1522	100.0	1522	US-09-968-007A-213	Sequence 213, App
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ALIGNMENTS

RESULT 1
US-09-772-719-1
; Sequence 1, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-772,719
FILING DATE: 30-JAN-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-772-719-1

Query Match      100.0%; Score 1522; DB 9; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: NM Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentl Ver. 2.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
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NAME/KEY: mat_peptide
LOCATION: (124)..(1389)
US-09-967-237-1

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Best Local Similarity 100.0%; Pred. No. 0;
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US-10-795-933-5
Sequence 5, Application US/10795933
Publication No. US20040259126A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021-2
CURRENT APPLICATION NUMBER: US/10/795,933
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US/08/260,190
PRIOR FILING DATE: 1994-06-15
PRIOR APPLICATION NUMBER: 08/177,093
PRIOR FILING DATE: 1993-12-30
PRIOR APPLICATION NUMBER: 07/964,589
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: PV-709-92
PRIOR FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (124)..(1389)
US-10-795-933-5

TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-888-694-1

Query Match 100.0%; Score 1522; DB 18; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 GACCAAGAGTCATTGGGCTATGAGAGGCAACCGCCCTGGCCCGGGGTGCCCAAGCTGC 480
421 GACCAAGAGTCATTGGGCTATGAGAGGCAACCGCCCTGGCCCGGGGTGCCCAAGCTGC 480
481 GGGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGGCC 540
481 GGGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGGCC 540
541 GGGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGGCC 600
541 GGGGGCCGCTTCAAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGGCC 600
601 AACCAATGGCAGAGTGTGCACTGACCTGTGCTCTGAGCTAGAGATGCTGTGGTCCC 660
601 AACCAATGGCAGAGTGTGCACTGACCTGTGCTCTGAGCTAGAGATGCTGTGGTCCC 660
661 GGGGGGAGTACCGGGCTCTGCAAGCTGCACTGTGCACTGTGGGGGCTGTGAGTGTCCGGCC 720
661 GGGGGGAGTACCGGGCTCTGCAAGCTGCACTGTGCACTGTGGGGGCTGTGAGTGTCCGGCC 720
721 TCGGAGCACTGTGAGAGGCAACGTTCCCGGAGATCAAGTGTGTTCAACCTCAGC 780
721 TCGGAGCACTGTGAGAGGCAACGTTCCCGGAGATCAAGTGTGTTCAACCTCAGC 780
781 ACCGCTTTGCGAGAGTGAAGAGGCTTGGGGCCGCGGAGAGGCTTGGCCCGGTGGCC 840
781 ACCGCTTTGCGAGAGTGAAGAGGCTTGGGGCCGCGGAGAGGCTTGGCCCGGTGGCC 840

841 GCCTTTCTGAGAGAGGCCCCGAGAGAAACAGTGCCTATGACAGTGTGCTGCTGCTTG 900
841 GCCTTTCTGAGAGAGGCCCCGAGAGAAACAGTGCCTATGACAGTGTGCTGCTGCTTG 900
901 GAAGAAATGCTGAGAGAGGCTCAGAGACTGAGGCTCCAGAGACTGAGACATATCTGACTC 960
901 GAAGAAATGCTGAGAGAGGCTCAGAGACTGAGGCTCCAGAGACTGAGACATATCTGACTC 960
961 CTGCTCTGACTTCAAGCGGCTTCACTTCCAAATATGAGGGGTCTGTGACTACCGGCTGT 1020
961 CTGCTCTGACTTCAAGCGGCTTCACTTCCAAATATGAGGGGTCTGTGACTACCGGCTGT 1020
1021 GCCCAGGAGTATCTGAGCTGATGTTTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1080
1021 GCCCAGGAGTATCTGAGCTGATGTTTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1080
1081 CACACCTCTCTGACACCTCTGAGGAGCTGTGTACTCTGAGCTACAGCTGAACCTTCGA 1140
1081 CACACCTCTCTGACACCTCTGAGGAGCTGTGTACTCTGAGCTACAGCTGAACCTTCGA 1140
1141 GCGAGGAGCTTTGAAATGAGGAGATGATGAGGCTCTTCTGCTGCTGAGTGAACAGC 1200
1141 GCGAGGAGCTTTGAAATGAGGAGATGATGAGGCTCTTCTGCTGCTGAGTGAACAGC 1200
1201 AGTCTCGGGGCTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1260
1201 AGTCTCGGGGCTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1260
1261 GCCCTGTTTGGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1261 GCCCTGTTTGGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1321 AGGAGCAGCAGAGAGGAGAAACAAAGGGGCTGAGCTACCGCCAGCAGAGGTAAGCCGAG 1380
1321 AGGAGCAGCAGAGAGGAGAAACAAAGGGGCTGAGCTACCGCCAGCAGAGGTAAGCCGAG 1380
1381 ACTGAGGCTTGAAGCTGATTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1440
1381 ACTGAGGCTTGAAGCTGATTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1440
1441 GAGGCGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 GAGGCGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 TTTTAAATTAATTTTAAAT 1522
1501 TTTTAAATTAATTTTAAAT 1522

RESULT 5
US-09-954-456-89
Sequence 89, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26

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; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 89
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-89

Query Match      100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAGTCAGCCGATGCTCCCTGTGCCCCAGCCCTGCTCTCTGTGATCCCGGCC 60
DB      31  ACAGTCAGCCGATGCTCCCTGTGCCCCAGCCCTGCTCTCTGTGATCCCGGCC 90
QY      61  CCTGCTCCAGGCTCACTGTGCACTGTGCTGTCACTGTGCTTCTGATGCTGTCCAT 120
DB      91  CCTGCTCCAGGCTCACTGTGCACTGTGCTGTCACTGTGCTTCTGATGCTGTCCAT 150
QY      121  CCCGAGAGGTTCCCGGATGAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGAGAA 180
DB      151  CCCGAGAGGTTCCCGGATGAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGAGAA 210
QY      181  GATGACCCACTGCGGCGAGAGAGATCTGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 240
DB      211  GATGACCCACTGCGGCGAGAGAGATCTGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 270
QY      241  CAACCCGAGAGAGAGATTTACTTGAAGAGAGATTTACTCTGAGAGAGAGATTTACTCT 300
DB      271  CAACCCGAGAGAGAGATTTACTTGAAGAGAGATTTACTCTGAGAGAGAGATTTACTCT 330
QY      301  GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTGAAGATTTACTCTGTT 360
DB      331  GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTGAAGATTTACTCTGTT 390
QY      361  GAGGCTCTGAGATCTCTCAAGAACCCCAAGATTAATGCCACAGAGAGAGAGAGAT 420
DB      391  GAGGCTCTGAGATCTCTCAAGAACCCCAAGATTAATGCCACAGAGAGAGAGAGAT 450
QY      421  GACCAAGATCTGAGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
DB      451  GACCAAGATCTGAGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 510
QY      481  GCGGCGCGCTTCCAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGAGCC 540
DB      511  GCGGCGCGCTTCCAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTTCGCCGAGCC 570
QY      541  CTGCGCGCTTGAATCTCTGAGGCTTCCAGCTTCGCGGCTCCCAAGATCTGCGGCT 600
DB      571  CTGCGCGCTTGAATCTCTGAGGCTTCCAGCTTCGCGGCTCCCAAGATCTGCGGCT 630
QY      601  AACCAATGCGCAAGTGTGCACTGACCCCTGCTCTGAGGCTGAAGATGCTGTGGGTCC 660
DB      631  AACCAATGCGCAAGTGTGCACTGACCCCTGCTCTGAGGCTGAAGATGCTGTGGGTCC 690
QY      661  GGGCGGAGATACCGGCTCTGAGGCTGATCTGCACTGAGGAGGCTGCAAGTGTGTCGG 720
DB      691  GGGCGGAGATACCGGCTCTGAGGCTGATCTGCACTGAGGAGGCTGCAAGTGTGTCGG 750
QY      721  TCGGAGCACTGTGGAAGGCAACCGTTTCCCTGCCAGATCACTGTGTTCACTCTGAC 780
DB      751  TCGGAGCACTGTGGAAGGCAACCGTTTCCCTGCCAGATCACTGTGTTCACTCTGAC 810
QY      781  ACCGCTTTCGCAAGATTTGACAGAGGCTTGGGGCCCGGAGAGGCTGTGGCCGTGGCC 840
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DB      811  ACCGCTTTCGCAAGATTTGACAGAGGCTTGGGGCCCGGAGAGGCTGTGGCCGTGGCC 870
QY      841  GCGCTTCTGAGAGAGGCGCCGAGAGAAACAGTGCTTATGAGAGATGCTGTGCTGCTG 900
DB      871  GCGCTTCTGAGAGAGGCGCCGAGAGAAACAGTGCTTATGAGAGATGCTGTGCTGCTG 930
QY      901  GAGGAATCGCTGAGAGAGGCTCAGAGACTAGAGTCCAGAGACTGAGACATATCTGACTC 960
DB      931  GAGGAATCGCTGAGAGAGGCTCAGAGACTAGAGTCCAGAGACTGAGACATATCTGACTC 990
QY      961  CTGCGCTTGAATTCAGCGGCTACTTCCAAATATGAGGAGGCTCTGATCAACCGGCTGT 1020
DB      991  CTGCGCTTGAATTCAGCGGCTACTTCCAAATATGAGGAGGCTCTGATCAACCGGCTGT 1050
QY      1021  GCCCAGGCTCATCTGAGTGTGTTTAAACAGACAGATGATGCTGATGAAGAGCTC 1080
DB      1051  GCCCAGGCTCATCTGAGTGTGTTTAAACAGACAGATGATGCTGATGAAGAGCTC 1110
QY      1081  CACACCTCTCTGACACCTGTGAGGACCTGATGATCTCTGAGCTACAGCTGAATTCGGA 1140
DB      1111  CACACCTCTCTGACACCTGTGAGGACCTGATGATCTCTGAGCTACAGCTGAATTCGGA 1170
QY      1141  GCGAGCGAGCCTTTGAATGAGGCGAGATGATGAGGCTCTCTCTGAGAGTGAAGAGC 1200
DB      1171  GCGAGCGAGCCTTTGAATGAGGCGAGATGATGAGGCTCTCTCTGAGAGTGAAGAGC 1230
QY      1201  AGTCTCTGAGGCTGATGAGCCAGTCACTGATTTCTGCTGAGCTGATGATCTCTCTA 1260
DB      1231  AGTCTCTGAGGCTGATGAGCCAGTCACTGATTTCTGCTGAGCTGATGATCTCTCTA 1290
QY      1261  GCGCTGTTTGGCTCTCTTTTGTGCTGACACAGGCTGCGTCTCTTGTGCAATGAGA 1320
DB      1291  GCGCTGTTTGGCTCTCTTTTGTGCTGACACAGGCTGCGTCTCTTGTGCAATGAGA 1350
QY      1321  AGGCAACAAGAGGAGAACCAAGGGGCTGAGCTACCGCCAGAGAGAGTGGCCGAG 1380
DB      1351  AGGCAACAAGAGGAGAACCAAGGGGCTGAGCTACCGCCAGAGAGAGTGGCCGAG 1410
QY      1381  ACTGAGGCTTGAAGAGGCTGATCTTGAAGATGATGAGAGCCAGAGAGAGATCTGAGG 1440
DB      1411  ACTGAGGCTTGAAGAGGCTGATCTTGAAGATGATGAGAGCCAGAGAGAGATCTGAGG 1470
QY      1441  GAGCGGCTTAACTGCTCTGCTGCTGATTTATGCACTTCTTTTAACTGCCAAGAAAT 1500
DB      1471  GAGCGGCTTAACTGCTCTGCTGCTGATTTATGCACTTCTTTTAACTGCCAAGAAAT 1530
QY      1501  TTTTAAATTAATTTATTAAT 1522
DB      1531  TTTTAAATTAATTTATTAAT 1552

RESULT 6
US-09-954-456-726
; Sequence 726, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE REFERENCE: 689290-76
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
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PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 726
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-726

Query Match 100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCCGCAATGCTCCCTGTCGCCCCAGCCCTGCTCTGTTGATCCCGCC 60
31 ACAGTCAGCCGCAATGCTCCCTGTCGCCCCAGCCCTGCTCTGTTGATCCCGCC 90
61 CCGTCCGAGGCTCTGTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
91 CCGTCCGAGGCTCTGTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
121 CCCGAGAGTGGCCCGGATGCAAGAGATTCCCTTGGAGAGAGCTCTTCTGGGAA 180
151 CCCGAGAGTGGCCCGGATGCAAGAGATTCCCTTGGAGAGAGCTCTTCTGGGAA 210
181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACTCAGAGAGAGAT 240
211 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTCACTCAGAGAGAGAT 270
241 CCAACCGGAGAGAGATCTGCTGAGAGAGAGATCTGCTGAGAGAGAGATCTGCT 300
271 CCAACCGGAGAGAGATCTGCTGAGAGAGAGATCTGCTGAGAGAGAGATCTGCT 330
301 GAAGTTAAGCTTAATCAGAGAGAGAGCTCCCTGAAGTGAAGATCTAATCTGTT 360
331 GAAGTTAAGCTTAATCAGAGAGAGAGCTCCCTGAAGTGAAGATCTAATCTGTT 390
361 GAAGCTCTGAGAGATCTGAGAAACCCAGAAATATGCCCAAGGACAAAGAGAGAT 420
391 GAAGCTCTGAGAGATCTGAGAAACCCAGAAATATGCCCAAGGACAAAGAGAGAT 450
421 GACCAAGATCTGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 480
451 GACCAAGATCTGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 510
481 GCGGCGCGCTTCAAGTCCCGGAGATATCCGCGCCAGCTGCGCTTCTGCGCGCC 540
511 GCGGCGCGCTTCAAGTCCCGGAGATATCCGCGCCAGCTGCGCTTCTGCGCGCC 570
541 CTGCGCGCCCTGGAATCTCTGGGCTTCAAGCTCCCGCTCCAGAACTGCGCGCC 600
571 CTGCGCGCCCTGGAATCTCTGGGCTTCAAGCTCCCGCTCCAGAACTGCGCGCC 630
601 AACCAATGCGCAAGTGTGCACTGACCTGCTCTGCGGCTGAGAGATGCTGCGGTC 660
631 AACCAATGCGCAAGTGTGCACTGACCTGCTCTGCGGCTGAGAGATGCTGCGGTC 690
661 GCGGCGGAGATACCGGCTCTGAGCTGCACTGCACTGCGGCGGCTGCAAGTCTG 720
691 GCGGCGGAGATACCGGCTCTGAGCTGCACTGCACTGCGGCGGCTGCAAGTCTG 750
721 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCGAGATTCACGTGTTCACTCAG 780
751 TCGAGACACACTGTGAGAGGCCACCGTTTCCCTGCGAGATTCACGTGTTCACTCAG 810

781 ACCGCTTGGCAGAGTTGACGAGGCTTGGGCGCCCGGAGAGGCTGCGCTGTTGGCC 840
811 ACCGCTTGGCAGAGTTGACGAGGCTTGGGCGCCCGGAGAGGCTGCGCTGTTGGCC 870
841 GCGCTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGACAGATGCTGCTGCTG 900
871 GCGCTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATGACAGATGCTGCTGCTG 930
901 GAGAAATGCTGAGAGAGGCTCAGAGATCTGAGTCCAGAGCTGAGACATATCTGACT 960
931 GAGAAATGCTGAGAGAGGCTCAGAGATCTGAGTCCAGAGCTGAGACATATCTGACT 990
961 CTGCGCTGAGCTTGAAGCGCTACTTCAATATGAGGAGGCTCTGACTACAGCGCTGT 1020
991 CTGCGCTGAGCTTGAAGCGCTACTTCAATATGAGGAGGCTCTGACTACAGCGCTGT 1050
1021 GCCCAGAGTGTATCTGATCTGATGTTTAAACAGACATGATCTGATCTGATGATCT 1080
1051 GCCCAGAGTGTATCTGATCTGATGTTTAAACAGACATGATCTGATCTGATGATCT 1110
1081 CACACCTCTCTGACACCTCTGAGGAGCTGCTGATCTGCTGCTGATGATCTGCTG 1140
1111 CACACCTCTCTGACACCTCTGAGGAGCTGCTGATCTGCTGCTGATGATCTGCTG 1170
1141 GCGAGCAGCCTTTGAAATGAGGAGATGATGAGGCTCTGCTGCTGAGAGAGAG 1200
1171 GCGAGCAGCCTTTGAAATGAGGAGATGATGAGGCTCTGCTGCTGAGAGAGAG 1230
1201 AGTCTCGGCTGCTGAGCAGTCTGAGTGAATCTGCTGCTGCTGCTGCTGATCTG 1260
1231 AGTCTCGGCTGCTGAGCAGTCTGAGTGAATCTGCTGCTGCTGCTGCTGATCTG 1290
1261 GCGCTGCTTGTGCTCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1291 GCGCTGCTTGTGCTCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
1321 AGGCAAGCAGAGAGGAGAAACAAAGGAGGAGTGAAGTACCGCCAGAGAGAGAG 1380
1351 AGGCAAGCAGAGAGGAGAAACAAAGGAGGAGTGAAGTACCGCCAGAGAGAGAG 1410
1381 ACTGAGCTTGAAGGCTGATCTTGAAGATGAGAAACCAAGCAGAGAGATCTGAGG 1440
1411 ACTGAGCTTGAAGGCTGATCTTGAAGATGAGAAACCAAGCAGAGAGATCTGAGG 1470
1441 GAGCGGCTAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1471 GAGCGGCTAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1530
1501 TTTTAAATAATATTTAAT 1522
1531 TTTTAAATAATATTTAAT 1552

RESULT 7
US-09-960-706-1080
Sequence 1080, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
APPLICANT: Manger, William B.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1080
LENGTH: 1552

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: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
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: OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080

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Query Match 1522;	100.0%;	Score 1522;	DB 10;	Length 1552;
Best Local Similarity		Pred. No. 0;		
Matches 1522;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	ACAGTGAAGCGCATGAGCTCCCTGTGACCCCAACCCCTGGATCCCTCTGTATATCCCGACC	60
Db	31	ACAGTGAAGCGCATGAGCTCCCTGTGACCCCAACCCCTGGATCCCTCTGTATATCCCGACC	90
Qy	61	CGTGTCCAGGCTCACTGTGCACCTGTCTGTCACTGTGTCTTGTAGTCCGTTCAT	120
Db	91	CGTGTCCAGGCTCACTGTGCACCTGTCTGTCACTGTGTCTTGTATCCGTTCAT	150
Qy	121	CCCCAAGGTTGGCCCCGGATTCGAGAGGATTTCCCCCTTGGAGAGAGGCTCTTCTGGGAA	180
Db	151	CCCCAAGGTTGGCCCCGGATTCGAGAGGATTTCCCCCTTGGAGAGAGGCTCTTCTGGGAA	210
Qy	181	GATGACCACTGGGCGAGAGGATCTGGCCAGTGAAGAAGATTCACCCCAGAGAGAGAT	240
Db	211	GATGACCACTGGGCGAGAGGATCTGGCCAGTGAAGAAGATTCACCCCAGAGAGAGAT	270
Qy	241	CAACCCGAGAGAGGATCTACCTGTGAGAGAGATCTACCTGTGAGAGAGATCTACCT	300
Db	271	CAACCCGAGAGAGGATCTACCTGTGAGAGAGATCTACCTGTGAGAGAGATCTACCT	330
Qy	301	GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTACCTAATGTT	360
Db	331	GAAGTTAAGCTTAATCAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTACCTAATGTT	390
Qy	361	GAGGCTCTGTGAGATCTCTCAAGAACCCCAAGATTATGCCCCAGGGACAAGAGAGGAT	420
Db	391	GAGGCTCTGTGAGATCTCTCAAGAACCCCAAGATTATGCCCCAGGGACAAGAGAGGAT	450
Qy	421	GACAGAGTCAATTGGGCTTGAAGGCGAACCCGCTGTGGCCCGGATGTCCCAAGCTTGC	480
Db	451	GACAGAGTCAATTGGGCTTGAAGGCGAACCCGCTGTGGCCCGGATGTCCCAAGCTTGC	510
Qy	481	GCGGGCCGCTTCAATGCCCGGTGATATCCGCCCCAGCTTGCCTGCGCTTTCGCCGGCC	540
Db	511	GCGGGCCGCTTCAATGCCCGGTGATATCCGCCCCAGCTTGCCTGCGCTTTCGCCGGCC	570
Qy	541	CTGCGGCCCTGTGAATCTCTGTGGATTCAAGCTCCGCGCGCTCCAGAACCTGTGGCTTGGC	600
Db	571	CTGCGGCCCTGTGAATCTCTGTGGATTCAAGCTCCGCGCGCTCCAGAACCTGTGGCTTGGC	630
Qy	601	AACAAATGGCCACAGTGTGCACCTGAACCTTGCCTCTGTGGCTTGAAGATGTGCTTGGATCCC	660
Db	631	AACAAATGGCCACAGTGTGCACCTGAACCTTGCCTCTGTGGCTTGAAGATGTGCTTGGATCCC	690
Qy	661	GGGCGGGAATACCGGGCTTGTGACGCTGCATCTGTGCTGGGGGCTGCAAGTCTGTCCGGCC	720
Db	691	GGGCGGGAATACCGGGCTTGTGACGCTGCATCTGTGCTGGGGGCTGCAAGTCTGTCCGGCC	750
Qy	721	TGGAACACACTGTGTGAAGGCAACGTTTCCCTGCGAGATTCACAGTGTTCACCTAGC	780
Db	751	TGGAACACACTGTGTGAAGGCAACGTTTCCCTGCGAGATTCACAGTGTTCACCTAGC	810
Qy	781	ACCGCTTTTGCAGAGTTTACAGAGGCTTGTGGGCGCCCGGAGAGGCTTGGCCGTTTGGCC	840
Db	811	ACCGCTTTTGCAGAGTTTACAGAGGCTTGTGGGCGCCCGGAGAGGCTTGGCCGTTTGGCC	870
Qy	841	GCTTTTCTGAGAGAGGCGCCGAGAGAAAACAGTGTATATGACAGTTGTCTGTCTGCTTG	900
Db	871	GCTTTTCTGAGAGAGGCGCCGAGAGAAAACAGTGTATATGACAGTTGTCTGTCTGCTTG	930
Qy	901	GAAAGAAATGGCTGAAGAAAGGCTCAAGACTCAAGATCCAGAGCTGTGCATATCTGCATTC	960
Db	931	GAAAGAAATGGCTGAAGAAAGGCTCAAGACTCAAGATCCAGAGCTGTGCATATCTGCATTC	990

Qy	961	CTGCCCTCTGACTTCACACCGTACTTCCAAATATGAGGGGCTCTGACTAACCGCCCTGT	1020
Db	991	CTGCCCTCTGACTTCACACCGCTACTTCCAAATATGAGGGGCTCTGACTAACCGCCCTGT	1050
Qy	1021	GCCCAAGGGTGCATCTGGACTGTGTATTAACACAGACAGTGAATGCTGAATGCTAAACAGCTC	1080
Db	1051	GCCCAAGGGTGCATCTGGACTGTGTATTAACACAGACAGTGAATGCTGAATGCTAAACAGCTC	1110
Qy	1081	CACACCTCTCTGACACCCCTGTGGGAACTGTGTGACTCTCTGGGTACACGCTGAACCTTCCGA	1140
Db	1111	CACACCTCTCTGACACCCCTGTGGGAACTGTGTGACTCTCTGGGTACACGCTGAACCTTCCGA	1170
Qy	1141	GCGACGAGCCTTTGAATGAGGACAGTAAATGAGGCGCTCTTCCCTGCTGAGATGGAACAGC	1200
Db	1171	GCGACGAGCCTTTGAATGAGGACAGTAAATGAGGCGCTCTTCCCTGCTGAGATGGAACAGC	1230
Qy	1201	AGTCCTTGAGGCTGTGACGACAGTCCAGCTGAATTTCTGCTGAGCTGTGTGATCATCTTA	1260
Db	1231	AGTCCTTGAGGCTGTGACGACAGTCCAGCTGAATTTCTGCTGAGCTGTGTGATCATCTTA	1290
Qy	1261	GCCCTGGTTTTTGGCCCTCTTTTGGCTGTCAACAGGCTGCCGTTCCTTGTGACAGATGAGA	1320
Db	1291	GCCCTGGTTTTTGGCCCTCTTTTGGCTGTCAACAGGCTGCCGTTCCTTGTGACAGATGAGA	1350
Qy	1321	AGGCAGACAGAAAGGGGAAACCAAAGGGGGGTGATGACATACGAGCCACAGAGGTAAAGCGAG	1380
Db	1351	AGGCAGACAGAAAGGGGAAACCAAAGGGGGGTGATGACATACGAGCCACAGAGGTAAAGCGAG	1410
Qy	1381	ACTGGAACCTTAGAGGCTGATCTTGTGAGAAATGTGAGAAAGCCACGACAGAGCATCTGAGGG	1440
Db	1411	ACTGGAACCTTAGAGGCTGATCTTGTGAGAAATGTGAGAAAGCCACGACAGAGCATCTGAGGG	1470
Qy	1441	GGAACCGGTAACTGTCTGTCTGCTCATTAATGCACTTCTTTTAACTGCGCAAGAAATT	1500
Db	1471	GGAACCGGTAACTGTCTGTCTGCTCATTAATGCACTTCTTTTAACTGCGCAAGAAATT	1530
Qy	1501	TTTTAAATTAATATTTATTAAT	1522
Db	1531	TTTTAAATTAATATTTATTAAT	1552

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RESULT 8
US-09-873-367C-516
; Sequence 516, Application US/09873367C
; Publication No. US20030165839A1
GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIORITY APPLICATION NUMBER: U.S. 60/236,891
PRIORITY FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: U.S. 60/236,842
PRIORITY FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: U.S. 60/244,867
PRIORITY FILING DATE: 2000-11-01
PRIORITY APPLICATION NUMBER: U.S. 60/245,084
PRIORITY FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0
SEQ ID NO 516
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-873-367C-516

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Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCGGATGCTCCCTGTGTCACGAGCCCTGCTCCTCTGTGATCCCGGCC 60
Db 31 ACAGTCAGCGGATGCTCCCTGTGTCACGAGCCCTGCTCCTCTGTGATCCCGGCC 90

Qy 61 CTTGCTCCAGGCTCTCATCTGTGCACTGTCTGTCTCATCTGTCTGTGATGCTGTCCAT 120
Db 91 CTTGCTCCAGGCTCTCATCTGTGCACTGTCTGTCTCATCTGTCTGTGATGCTGTCCAT 150

Qy 121 CCCCAAGGTTGGCCCGGATGTCAGAGGATGTCCTCCCTGTGGAGAGGCTCTTCTGGGGA 180
Db 151 CCCCAAGGTTGGCCCGGATGTCAGAGGATGTCCTCCCTGTGGAGAGGCTCTTCTGGGGA 210

Qy 181 GATGACCCACTGAGGCGAGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 240
Db 211 GATGACCCACTGAGGCGAGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 270

Qy 241 CCAACCCGAGAGAGATCTTACTGTGAGAGAGATCTTACTGTGAGAGAGATCTTACT 300
Db 271 CCAACCCGAGAGAGATCTTACTGTGAGAGAGATCTTACTGTGAGAGAGATCTTACT 330

Qy 301 GAAGTTAAGCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGATCTTACTACTGTT 360
Db 331 GAAGTTAAGCTTAATCAGAGAGAGGCTCCCTGAAGTTAGAGATCTTACTACTGTT 390

Qy 361 GAGGCTCTGTGAGATCTCTAAGAACCCAGAAATATGCCACAGGACAAAGAGAGGAT 420
Db 391 GAGGCTCTGTGAGATCTCTAAGAACCCAGAAATATGCCACAGGACAAAGAGAGGAT 450

Qy 421 GACGAGATCTATGGGCTATGAGAGGCAACCGGCTTGGCCCGGGTGTCCCAAGCTTCG 480
Db 451 GACGAGATCTATGGGCTATGAGAGGCAACCGGCTTGGCCCGGGTGTCCCAAGCTTCG 510

Qy 481 GGGGGCGGCTTCAAGTCCCGGATGATCCCGGCTGAGCTGCGGCTTCTGCGCGGCC 540
Db 511 GGGGGCGGCTTCAAGTCCCGGATGATCCCGGCTGAGCTGCGGCTTCTGCGCGGCC 570

Qy 541 CTGCGCCCTGTGAATCTCTGTGGCTTTCAGCTCCCGCGCTCCAGAACTGCGGCTGCGC 600
Db 571 CTGCGCCCTGTGAATCTCTGTGGCTTTCAGCTCCCGCGCTCCAGAACTGCGGCTGCGC 630

Qy 601 AACATGCGCACTGTGCACTGACCTGCTCTGCTGCTGAGATGCTCTGCTGCTCC 660
Db 631 AACATGCGCACTGTGCACTGACCTGCTCTGCTGCTGAGATGCTCTGCTGCTCC 690

Qy 661 GGGCGGAGTACCGGCTGTGCACTGCACTGCACTGCGGGGCTGCAAGTGTCCGGGC 720
Db 691 GGGCGGAGTACCGGCTGTGCACTGCACTGCACTGCGGGGCTGCAAGTGTCCGGGC 750

Qy 721 TCGAGACACTGTGAGAGGCAACGCTTCCCTGCGAGATTCACGCTGTTCACTCAGC 780
Db 751 TCGAGACACTGTGAGAGGCAACGCTTCCCTGCGAGATTCACGCTGTTCACTCAGC 810

Qy 781 ACCGCTTTGCAAGTGAACGAGGCTTGGGGCGCCGAGAGGCTGCGCTGTTGGCC 840
Db 811 ACCGCTTTGCAAGTGAACGAGGCTTGGGGCGCCGAGAGGCTGCGCTGTTGGCC 870

Qy 841 GCTTTTGTGAGAGAGGCGCGAGAAACAGTGCCTATGAGAGATGTTGCTCGCTTG 900
Db 871 GCTTTTGTGAGAGAGGCGCGAGAAACAGTGCCTATGAGAGATGTTGCTCGCTTG 930

Qy 901 GAAGAAATGCTGAGAGAGGCTCAGAGATCAGATCCAGAGACTGAGCAATCTGCACTC 960
Db 931 GAAGAAATGCTGAGAGAGGCTCAGAGATCAGATCCAGAGACTGAGCAATCTGCACTC 990

Qy 961 CTGCGCTGTGATCTTCAAGCGCTATCTTCAATATGAGGGGCTTCTGATCAACCGGCTGT 1020
Db 991 CTGCGCTGTGATCTTCAAGCGCTATCTTCAATATGAGGGGCTTCTGATCAACCGGCTGT 1050

Qy 1021 GCCCAGGCTGATCTGAGCTGTGTTTAAACAGAGATGATCTGAGTCTAAGAGCTC 1080
Db 1051 GCCCAGGCTGATCTGAGCTGTGTTTAAACAGAGATGATCTGAGTCTAAGAGCTC 1110

Qy 1081 CACACCTCTCTGACACCTCTGTGGGACCTGTGATCTTGGCTACAGCTGAACCTTCCGA 1140
Db 1111 CACACCTCTCTGACACCTCTGTGGGACCTGTGATCTTGGCTACAGCTGAACCTTCCGA 1170

Qy 1141 GCGAGCGAGCTTTAAATGGGAGATGATGAGGCTCCTTCCCTGTGAGATGAGCAGC 1200
Db 1171 GCGAGCGAGCTTTAAATGGGAGATGATGAGGCTCCTTCCCTGTGAGATGAGCAGC 1230

Qy 1201 AGTCTCGGAGCTGAGAGCAGTCCAGTGAATCTTCTGCTGCTGCTGCTGATCAATCTTA 1260
Db 1231 AGTCTCGGAGCTGAGAGCAGTCCAGTGAATCTTCTGCTGCTGCTGCTGATCAATCTTA 1290

Qy 1261 GCCCTGTTTGGCTCTCTTTTGTGTCACAGAGTGGCTTCTTGTGCAATGAGA 1320
Db 1291 GCCCTGTTTGGCTCTCTTTTGTGTCACAGAGTGGCTTCTTGTGCAATGAGA 1350

Qy 1321 AGGACGACAGAAAGGGAACCAAGGGGTGAGACTACCGGCCAGAGAGGTAGCCGAG 1380
Db 1351 AGGACGACAGAAAGGGAACCAAGGGGTGAGACTACCGGCCAGAGAGGTAGCCGAG 1410

Qy 1381 ACTGAGCCTAGAGCTGATCTTGAAGATGAGAAAGCCAGAGAGGATCTGAGGG 1440
Db 1411 ACTGAGCCTAGAGCTGATCTTGAAGATGAGAAAGCCAGAGAGGATCTGAGGG 1470

Qy 1441 GGAGCGGTACTGTCTGTCTCTCATTAATGCACTTCTTTTACTGCAAGAAAT 1500
Db 1471 GGAGCGGTACTGTCTGTCTCTCATTAATGCACTTCTTTTACTGCAAGAAAT 1530

Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 9
US-09-968-007A-213
Sequence 213, Application US/09968007A
GENERAL INFORMATION:
APPLICANT: Eber, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968, 007A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237, 172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237, 173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237, 278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237, 294
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237, 295
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237, 316
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PatencIn version 3.0
SEQ ID NO 213
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-213

Query Match 100.0%; Score 1522; DB 11; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGTCAGCGGATGCTCCCTGTGTCACGAGCCCTGCTCCTCTGTGATCCCGGCC 60

Db 1111 CACACCTCTCTGACACCTCTGAGGACCTGAGTACTCGGCTACAGCTGAATTCCGA 1170
Qy 1141 GCGAGCAGCCTTTGAATGAGCGAGATGATGAGGCTCTTCCCTGCTGAGGTGACAGC 1200
Db 1171 GCGAGCGAGCCTTTGAATGAGCGAGATGATGAGGCTCTTCCCTGCTGAGGTGACAGC 1230
Qy 1201 AGTCTCGGAGTCTGAGACCGAGTCCAGTGAATTCCTGCTGAGGTCTGAGTCTCTTA 1260
Db 1221 AGTCTCGGAGTCTGAGACCGAGTCCAGTGAATTCCTGCTGAGGTCTGAGTCTCTTA 1290
Qy 1261 GCCCTGTTTGGGCTCTTTTGTCTGTCAACAGCGTGGGCTTCTTGTGCAATGAGA 1320
Db 1291 GCCCTGTTTGGGCTCTTTTGTCTGTCAACAGCGTGGGCTTCTTGTGCAATGAGA 1350
Qy 1321 AGGAGCAGAGAGGAGAACCAAGGAGGTGAGCTACGCGCCAGCAGAGGTAGCGAG 1380
Db 1351 AGGAGCAGAGAGGAGAACCAAGGAGGTGAGCTACGCGCCAGCAGAGGTAGCGAG 1410
Qy 1381 ACTGAGCTTGAAGCTGAGTCTTGAAGAAATGTAGAAAGCCAGCCAGAGCATCGAGG 1440
Db 1411 ACTGAGCTTGAAGCTGAGTCTTGAAGAAATGTAGAAAGCCAGCCAGAGCATCGAGG 1470
Qy 1441 GAGCGGCTACTGCTGCTGCTCTCTCATATGCACTTCTTTAACTGCAAGAAATT 1500
Db 1471 GAGCGGCTACTGCTGCTGCTCTCTCATATGCACTTCTTTAACTGCAAGAAATT 1530
Qy 1501 TTTTAAATTAATTAATTAAT 1522
Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 10
US-10-301-822-11
; Sequence 11, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MP01-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43) ... (1422)
US-10-301-822-11

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCGCATGCTCCCTGTCGCCAGCCCTGAGTCTCCTGTTGATCCGCGCC 60

Qy 31 AAGATGAGCGATGCTCCCTGTCGCCAGCCCTGAGTCTCCTGTTGATCCGCGCC 90
Qy 61 CCTGCTCAGGCTCACTGTGCAACTGTCTGTCACTGTCTTCTGATGCTGTCCAT 120
Db 91 CTTGCTCAGGCTCACTGTGCAACTGTCTGTCACTGTCTTCTGATGCTGTCCAT 150
Qy 121 CCCCAGAGGTTGCCCCGATGCAAGAGATTTCCCTTTGGAGAGAGGCTCTTCTGGGAA 180
Db 151 CCCCAGAGGTTGCCCCGATGCAAGAGATTTCCCTTTGGAGAGAGGCTCTTCTGGGAA 210
Qy 181 GATGACCCCACTGGGCGAGAGATCTGCGCAGTGAAGAGATTTCACCCAAGAGAGAGAT 240
Db 211 GATGACCCCACTGGGCGAGAGATCTGCGCAGTGAAGAGATTTCACCCAAGAGAGAGAT 270
Qy 241 CCACCCGAGAGAGAGATCTACCTTGAGAGAGAGATCTACCTTGAGAGAGAGATCTACCT 300
Db 271 CCACCCGAGAGAGAGATCTACCTTGAGAGAGAGATCTACCTTGAGAGAGAGATCTACCT 330
Qy 301 GAAGTTAAGCTTAATCAGAAAGAGGCTCCCTGAAATTGAGAGATCTTACTTCTGTT 360
Db 331 GAAGTTAAGCTTAATCAGAAAGAGGCTCCCTGAAATTGAGAGATCTTACTTCTGTT 390
Qy 361 GAGGCTCCTGAGATCTTCAAGAACCCCAAGATTAATGCCACAGGAGCAAGAGGAGAT 420
Db 391 GAGGCTCCTGAGATCTTCAAGAACCCCAAGATTAATGCCACAGGAGCAAGAGGAGAT 450
Qy 421 GACAGAGTCAATTGAGGCTATGAGAGCGACCCGCGCTGAGCCCGGAGTCCCAACCTGC 480
Db 451 GACAGAGTCAATTGAGGCTATGAGAGCGACCCGCGCTGAGCCCGGAGTCCCAACCTGC 510
Qy 481 GGGGCGGCTTCAAGTCCCGGTGATATCCGCGCTCCAGCTGCGGCTTCTGCGCGGC 540
Db 511 GGGGCGGCTTCAAGTCCCGGTGATATCCGCGCTCCAGCTGCGGCTTCTGCGCGGC 570
Qy 541 CCGCGCCCTGGAATCTCTGAGGCTTCCAGCTCCGCGCTCCCAAACTGCGCTGCGC 600
Db 571 CCGCGCCCTGGAATCTCTGAGGCTTCCAGCTCCGCGCTCCCAAACTGCGCTGCGC 630
Qy 601 AACAAATGCGCAGTGTGCACTGACCTGCTCTGAGGCTGAGAGATGCTGAGGCTCC 660
Db 631 AACAAATGCGCAGTGTGCACTGACCTGCTCTGAGGCTGAGAGATGCTGAGGCTCC 690
Qy 661 GGGCGGAGTACCGGCTCTGAGGCTGAGCTGAGCTGAGGCGGCTGAGGCTGCGCGC 720
Db 691 GGGCGGAGTACCGGCTCTGAGGCTGAGCTGAGCTGAGGCGGCTGAGGCTGCGCGC 750
Qy 721 TCGAGCACACTGTGGAAGGCGACCGTTTCCCTGCGAGATCCAGTGTTCACCTCAGC 780
Db 751 TCGAGCACACTGTGGAAGGCGACCGTTTCCCTGCGAGATCCAGTGTTCACCTCAGC 810
Qy 781 ACCGCTTTTGCAGAGTTGACGAGGCGCTTGGGCGCGCGGAGGCTGCTGTTGCGC 840
Db 811 ACCGCTTTTGCAGAGTTGACGAGGCGCTTGGGCGCGCGGAGGCTGCTGTTGCGC 870
Qy 841 GCTTTCTGAGAGAGGCGCGGAGAAACAATGCTATGACAGTGTGCTGCTGCTG 900
Db 871 GCTTTCTGAGAGAGGCGCGGAGAAACAATGCTATGACAGTGTGCTGCTGCTG 930
Qy 901 GAAGAAATGCTGAGAGAGGCTCAGAGATCCAGTCCCGAGACTGAGACATCTGCACTC 960
Db 931 GAAGAAATGCTGAGAGAGGCTCAGAGATCCAGTCCCGAGACTGAGACATCTGCACTC 990
Qy 961 CTGCGCTCTGACTTCAAGCGGCTACTTCCAAATATGAGGAGGCTCTGACTACACCGCCTGT 1020
Db 991 CTGCGCTCTGACTTCAAGCGGCTACTTCCAAATATGAGGAGGCTCTGACTACACCGCCTGT 1050
Qy 1021 GCCCAGGAGTATCTGAGCTGTGTTTAAACGACAGATGATCTGAGGCTTAAAGAGCTC 1080
Db 1051 GCCCAGGAGTATCTGAGCTGTGTTTAAACGACAGATGATCTGAGGCTTAAAGAGCTC 1110
Qy 1081 CACACCTCTCTGACACCTGTGAGGAGCTGAGTCTCGGCTACAGCTGAATCTCCGA 1140

OY	241	CCACCCGGAGAGAGATTTACTCTGGAGAGAGATCTACCTGGAGAGAGAGATCTACCT	300
Db	271	CCACCCGGAGAGAGATTTACTCTGGAGAGAGATCTACCTGGAGAGAGATCTACCT	330
OY	301	GAAGTTAAGCTTAAATCAGAGAAGAGGGCTCCCTGAAGTTAAGAGATCTTACTGT	360
Db	331	GAAGTTAAGCTTAAATCAGAGAAGAGGGCTCCCTGAAGTTAAGAGATCTTACTGT	390
OY	361	GAGGCTCCTGGAGATCTCTCAAGACCCCGAATTAATGCCCAAGGGACAAAGAAGGAGT	420
Db	391	GAGGCTCCTGGAGATCTCTCAAGACCCCGAATTAATGCCCAAGGGACAAAGAAGGAGT	450
OY	421	GAACCAAGTCATTGCGCTATGAGGCGACCCGCCCTGGCCCCGGGTGTCCCAAGCTGC	480
Db	451	GAACCAAGTCATTGCGCTATGAGGCGACCCGCCCTGGCCCCGGGTGTCCCAAGCTGC	510
OY	481	GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCAGCTGGCGGCTTTGCCCCGAGC	540
Db	511	GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCAGCTGGCGGCTTTGCCCCGAGC	570
OY	541	CTGCGCCCCCTGGAATCCTTGAGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTGCG	600
Db	571	CTGCGCCCCCTGGAATCCTTGAGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTGCG	630
OY	601	AACAATGGCCACAGTGTGCACTGAACCTTGCTCTTGAGTGAAGATGCTTGAGGTCC	660
Db	631	AACAATGGCCACAGTGTGCACTGAACCTTGCTCTTGAGTGAAGATGCTTGAGGTCC	690
OY	661	GGGCGGAGATACCGGAGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTGTCCGGG	720
Db	691	GGGCGGAGATACCGGAGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTGTCCGGG	750
OY	721	TCGGAGCACACTGTGAGAAAGGCCACCGTTCCTCTGCGAGATCCAGTGTGTTCACTCAGC	780
Db	751	TCGGAGCACACTGTGAGAAAGGCCACCGTTCCTCTGCGAGATCCAGTGTGTTCACTCAGC	810
OY	781	ACCGGCTTGCACAGATTGACGAGGCTTTGGGGGCGCCGGAGAGGCTGGCGGTGTGGCC	840
Db	811	ACCGGCTTGCACAGATTGACGAGGCTTTGGGGGCGCCGGAGAGGCTGGCGGTGTGGCC	870
OY	841	GCCTTTCTGAGAGAGGGCCCGGAAAGAAACAGTGCCTATGACAGTTCGTCTGAGCTTG	900
Db	871	GCCTTTCTGAGAGAGGGCCCGGAAAGAAACAGTGCCTATGACAGTTCGTCTGAGCTTG	930
OY	901	GAAGAAATCGCTGAGAGAGAGGCTCAAGAGACTCAGGTGCCAGAGCTGACATATCTGCATC	960
Db	931	GAAGAAATCGCTGAGAGAGAGGCTCAAGAGACTCAGGTGCCAGAGCTGACATATCTGCATC	990
OY	961	CTGCGCTCTGACTTACGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACAACCGGCTGT	1020
Db	991	CTGCGCTCTGACTTACGCGGCTACTTCCAAATATGAGGGGTCTCTGACTACAACCGGCTGT	1050
OY	1021	GCCCAAGGATCATCTGGACTGTGTGTTTAAACAGACAGATGATGCTAAGTGTCAAGCACTC	1080
Db	1051	GCCCAAGGATCATCTGGACTGTGTGTTTAAACAGACAGATGATGCTAAGTGTCAAGCACTC	1110
OY	1081	CACACCCCTCTGACACCCCTGTGGGGAACTGTGTGACTCTCGGCTTCAAGTGAATCTCCGA	1140
Db	1111	CACACCCCTCTGACACCCCTGTGGGGAACTGTGTGACTCTCGGCTTCAAGTGAATCTCCGA	1170
OY	1141	GCGACGCAAGCTTTGAAATGAGGCGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGAAGC	1200
Db	1171	GCGACGCAAGCTTTGAAATGAGGCGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGAAGC	1230
OY	1201	AGTCTTGGGGGTGCTGAGCCAGTCCAGCTGAATTTCTGTGCTGGTCTGTGATCTCTTA	1260
Db	1231	AGTCTTGGGGGTGCTGAGCCAGTCCAGCTGAATTTCTGTGCTGGTCTGTGATCTCTTA	1290
OY	1261	GCCCTGATTTTGGGCTCTCTTTTCTGTGACACAGCTGCGGTTCTCTTGTGAGATGAGA	1320
Db	1291	GCCCTGATTTTGGGCTCTCTTTTCTGTGACACAGCTGCGGTTCTCTTGTGAGATGAGA	1350
OY	1321	AGGCAACAGAGAGGGAAACAAAGGGGGTGTAGCTACCGCCACAGAGAGTACCGAG	1380

Db	1351	AGCGACGACGAAAGGGGAAACCAAAAGGGGGGTGAGCTTCCGCCACGACGAGGTACCCAG	14110
QY	1381	ACTGAGCGCTAGAGGCTGATCTTGAGAAATGTGAGAACGACGACGAGCATCTGAGGG	14408
Db	1411	ACTGAGCGCTTAGAGGCTGATCTTGAGAAATGTGAGAAACGACGAGGCGATCTGAGGG	14707
QY	1441	GGAGCCGGTAACTGCTCTGCTCTGCTACTATTATGCACTTCTTTTAACTGCGCAAAATT	15008
Db	1471	GGAGCCGGTAACTGCTCTGCTCTCTATTATGCACTTCTTTTAACTGCGCAAAATT	15310
QY	1501	TTTTAAATTAATATTATTAAT	1522
Db	1531	TTTTAAATTAATATTATTAAT	1552

```

RESULT 12
US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yundong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernarde, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

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Query Match	100.0%	Score 1522;	DB 15;	Length 1552;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1522;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	ACAGTCAGGCGGATGAGCTCCCTGTGGCCCAAGCCCTGAGCTCCCTGTGGATCCGGGC	60
Db	31	ACAGTCAGGCGGATGAGCTCCCTGTGGCCCAAGCCCTGAGCTCCCTGTGGATCCGGGC	90
Qy	61	CCGTCTCCAGGCGCTCACTGTGCAATGCTGCTGTCACTGCTGCTTCTGATGCTGTTCAT	120
Db	91	CCGTCTCCAGGCGCTCACTGTGCAATGCTGCTGTCACTGCTGCTTCTGATGCTGTTCAT	150
Qy	121	CCCCAGAGGTTCCCGGATGAGAGGATTCCTCCCTTGAGAGAGGCTTTCTGGGGAA	180
Db	151	CCCCAGAGGTTCCCGGATGAGAGGATTCCTCCCTTGAGAGAGGCTTTCTGGGGAA	210
Qy	181	GATGATCCCACTGGGCGAGAGGATTTGCGCAGTGAAGGATTCACCCAAAGAGAGAT	240
Db	211	GATGATCCCACTGGGCGAGAGGATTTGCGCAGTGAAGGATTCACCCAAAGAGAGGAT	270
Qy	241	CCACCCCGAGAGAGGATCTACCTGGAAGAGGATCTACCTGGAAGAGGATCTACCT	300
Db	271	CCACCCCGAGAGAGGATCTACCTGGAAGAGGATCTACCTGGAAGAGGATCTACCT	330
Qy	301	GAAGTTAACTTAATTCAGAGAAAGAGGCTCCCTGAAGTTAGAGATCTAACCTACGT	360
Db	331	GAAGTTAACTTAATTCAGAGAAAGAGGCTCCCTGAAGTTAGAGATCTAACCTACGT	390

QY 361 GAGGCTCTGAGATCTCAAGAACCCAGAAATATGCCACAGGAGCAAGAGGGAT 420
 Db 391 GAGGCTCTGAGATCTCTCAAGAACCCAGAAATATGCCACAGGAGCAAGAGGGAT 450
 QY 421 GACCAAGTCATTTGGCGCTATGAGAGCCGCCCTTGGCCCCGGGTGCTCCCACTGC 480
 Db 451 GACCAAGTCATTTGGCGCTATGAGAGCCGCCCTTGGCCCCGGGTGCTCCCACTGC 510
 QY 481 GGGGGCCGCTTCAGTCCCGGTGATATCCGCCCCAGCTGCGGCTCTTGCCTGC 540
 Db 511 GGGGGCCGCTTCAGTCCCGGTGATATCCGCCCCAGCTGCGGCTCTTGCCTGC 570
 QY 541 CTGCGCCCCCTTGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGC 600
 Db 571 CTGCGCCCCCTTGAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGC 630
 QY 601 AACATGGCCACAGTGTGCACTGACCTTGCCTCTGGGCTTGAAGATGGCTCTGGGTCCC 660
 Db 631 AACATGGCCACAGTGTGCACTGACCTTGCCTCTGGGCTTGAAGATGGCTCTGGGTCCC 690
 QY 661 GGGGGGGATACCGGGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTGTGCTCCGGGC 720
 Db 691 GGGGGGGATACCGGGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTGTGCTCCGGGC 750
 QY 721 TCGGAGCACTGTGGAGGCCACCGCTTCTCCCTGCCAGATCCAGTGTGCTCACTCAAC 780
 Db 751 TCGGAGCACTGTGGAGGCCACCGCTTCTCCCTGCCAGATCCAGTGTGCTCACTCAAC 810
 QY 781 ACCGCTTTTGCAGAGTTGACAGAGGCTTGGGGGCGCCCGGAGGCGCTTGGCTTGGCC 840
 Db 811 ACCGCTTTTGCAGAGTTGACAGAGGCTTGGGGGCGCCCGGAGGCGCTTGGCTTGGCC 870
 QY 841 GCTTTTGGAGAGAGGGCCCGAGAAACAGTGGCTATGAGACAGTGTGCTGCTGCTG 900
 Db 871 GCTTTTGGAGAGAGGGCCCGAGAAACAGTGGCTATGAGACAGTGTGCTGCTGCTG 930
 QY 901 GAAGAAATGCTGAGAGAGGCTCAGAGACTCAGATCCAGACTGAGCAATATCTGCACTC 960
 Db 931 GAAGAAATGCTGAGAGAGGCTCAGAGACTCAGATCCAGACTGAGCAATATCTGCACTC 990
 QY 961 CTGCTCTGACTTCAAGCCGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
 Db 991 CTGCTCTGACTTCAAGCCGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
 QY 1021 GCGGAGGCTGATCTGAGCTGTGTTAACAGACAGTATGCTGAGTCTGAGAGAGCTC 1080
 Db 1051 GCGGAGGCTGATCTGAGCTGTGTTAACAGACAGTATGCTGAGTCTGAGAGAGCTC 1110
 QY 1081 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTCGGCTACAGCTGAATCTTCCGA 1140
 Db 1111 CACACCTCTCTGACACCTCTGTGGGAGCTGTGACTCTCGGCTACAGCTGAATCTTCCGA 1170
 QY 1141 GCGAGCGAGCTTTGAAATGGGCGAGTATGAGGCTCTTCTCTGCTGAGATGGAACAGC 1200
 Db 1171 GCGAGCGAGCTTTGAAATGGGCGAGTATGAGGCTCTTCTCTGCTGAGATGGAACAGC 1230
 QY 1201 AGTCTCTGGGCTGCTGAGCACTGCACTGAATCTCTGCTGCTGCTGCTGCTGCTGCT 1260
 Db 1231 AGTCTCTGGGCTGCTGAGCACTGCACTGAATCTCTGCTGCTGCTGCTGCTGCTGCT 1290
 QY 1261 GCGCTGCTTTTGGGCTCTTTTGGCTGCTGCAAGAGTGGCGCTCTTGTGAGATGAGA 1320
 Db 1291 GCGCTGCTTTTGGGCTCTTTTGGCTGCTGCAAGAGTGGCGCTCTTGTGAGATGAGA 1350
 QY 1321 AGGAGCACAAGAGGGGAAACAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
 Db 1351 AGGAGCACAAGAGGGGAAACAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410
 QY 1381 ACTGAGCTTAAGAGGCTGATCTTGGAGATGTGAGAACCCAGCCAGAGGACTTGAAGG 1440
 Db 1411 ACTGAGCTTAAGAGGCTGATCTTGGAGATGTGAGAACCCAGCCAGAGGACTTGAAGG 1470
 QY 1441 GAGAGCGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

Db 1471 GAGAGCGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
 QY 1501 TTTTAAATTAATTAATTAAT 1522
 Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 13
 US-10-388-360-291
 ; Sequence 291, Application US/10388360
 ; Publication No. US2003022528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GENOMIC HEALTH
 ; APPLICANT: Baker, Joffe B.
 ; APPLICANT: Cronin, Maureen T.
 ; APPLICANT: Klefer, Michael C.
 ; APPLICANT: Shak, Steve
 ; APPLICANT: Walker, Michael Graham
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
 ; FILE REFERENCE: 39740-0001US
 ; CURRENT APPLICATION NUMBER: US/10/388,360
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 60/412,049
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/364,890
 ; PRIOR FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 291
 ; LENGTH: 1552
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-388-360-291

Query Match 100.0%; Score 1522; DB 15; Length 1552;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 91 CTGCTCCAGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
 QY 121 CCCAGAGGTTGCCCGGATGAGAGGATTTCCCTTGGAGAGAGGCTTTCTGGGAA 180
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 QY 181 GATGACCACTGGGCGAGAGGATTTGCCCACTGAGAGATTCACCCAGAGAGAGAT 240
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 QY 241 CCAGCCGAGAGAGGATCTACCTGAGAGAGATCTACCTGAGAGAGGATCTACT 300
 Db 271 CCAGCCGAGAGAGGATCTACCTGAGAGAGATCTACCTGAGAGAGGATCTACT 330
 QY 301 GAAGTTAAGCCTTAATCAGAAAGAGGCTTCCCTGAAGTTAGAGATCTACTGTT 360
 Db 331 GAAGTTAAGCCTTAATCAGAAAGAGGCTTCCCTGAAGTTAGAGATCTACTGTT 390
 QY 361 GAGGCTCTGAGATCTTCAAGAACCCAGAAATATGCCACAGGAGCAAGAGGGAT 420
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 QY 421 GACCAAGTCATTTGGCGCTATGAGAGCCGCCCTTGGCCCCGGGTGCTCCCACTGC 480
 Db 451 GACCAAGTCATTTGGCGCTATGAGAGCCGCCCTTGGCCCCGGGTGCTCCCACTGC 510
 QY 481 GCGGGCCGCTTCAGTCCCGGTGATATCCGCCCCAGCTGCGGCTCTTGCCTGC 540

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Db	571	CTGGCCCCCTCCGGAATCTCTGGGCTTCGAGCTCCGCGCTCCCAAAATCGGCGCTGGCG	630
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Db	631	AACAAATGGCACAGTGTGCACTGACCCCTGCTCTGGGCTAGAGATGCTCTGGGCTCC	690
QY	661	GGGCGGGAATACCGGCTCTGCACTGCACTTGCACTGGGGGGCTGAGGTGTCGGGCG	720
Db	691	GGGCGGGAATACCGGCTCTGCACTGCACTTGCACTGGGGGGCTGAGGTGTCGGGCG	750
QY	721	TCGGAGCACTGTGGAAGGCAACCGTTTCCCTGCGGAGATCCACGTTGTTCACTCAG	780
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QY	781	ACCGCTTTTGCAGAGTTGACAGAGGCTTTGGGGGCGCCGGAGGCTCGGCGTGTGGCC	840
Db	811	ACCGCTTTTGCAGAGTTGACAGAGGCTTTGGGGGCGCCGGAGGCTCGGCGTGTGGCC	870
QY	841	GCGTTCTGGAGAGGAGGCGCGGAAAGAAACAGTGCTATGAGAGATGTCGTCTCCCTT	900
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QY	901	GAAGAATTCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGAGCTGGAACATATCGACCTC	960
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QY	1321	AGGCAGACAGAAAGGGGAACAAAGGGGGTGTGACTACGCCACAGAGTAAAGCCGAG	1380
Db	1351	AGGCAGACAGAAAGGGGAACAAAGGGGGTGTGACTACGCCACAGAGTAAAGCCGAG	1410
QY	1381	ACTGAGGCTTAAGGGCTGATCTTGAGAAATGTGAGAGCCAGCCAGAGGCACTTAAGGG	1440
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Db	1531	TTTTAAATTAATATTTATTAAT	1552

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: Sequence 305, Application US/10295027
: Publication No. US20030232350A1
: GENERAL INFORMATION:
: APPLICANT: Afari, Daniel
: APPLICANT: Aziz, Natasha
: APPLICANT: Ginsberg, Wendy M.
: APPLICANT: Gish, Kurt C.
: APPLICANT: Glynn, Richard
: APPLICANT: Hevez, Peter A.
: APPLICANT: Mack, David H.
: APPLICANT: Murray, Richard
: APPLICANT: Watson, Susan R.
: APPLICANT: Eos Biotechnology, Inc.
: TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
: TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
: FILE REFERENCE: 018501-012500US
: CURRENT APPLICATION NUMBER: US/10/295,027
: CURRENT FILING DATE: 2002-11-13
: PRIOR APPLICATION NUMBER: US 09/663,733
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: US 60/350,666
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/335,394
: PRIOR FILING DATE: 2001-11-15
: PRIOR APPLICATION NUMBER: US 60/332,464
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: US 60/334,393
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/340,376
: PRIOR FILING DATE: 2001-12-14
: PRIOR APPLICATION NUMBER: US 60/347,211
: PRIOR FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: US 60/347,349
: PRIOR FILING DATE: 2002-01-10
: PRIOR APPLICATION NUMBER: US 60/355,250
: PRIOR FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: US 60/356,714
: PRIOR FILING DATE: 2002-02-13
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 1386
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 305
: LENGTH: 1552
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-295-027-305
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: Query Match      100.0%; Score 1522; DB 15; Length 1552;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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: Db      31  AAGTCAAGCCGATGAGTCTCCCTGTGCCCCAGCCCCCTGAGCTCCCTGTGTGATCCCGGCC 90
: QY      61  CCTGCTCAGGCTCACTGTCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 120
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: QY      121  CCCCAGAGGTTGCCCCGGATGACAGAGAGATTCCCTTTGGAGAGAGGCTCTTCTGGGANA 180
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: QY      181  GATACACCACTGGGCGAGAGAGATCTGGCCAGTGAAGAGATTACCCAGAGAGAGAT 240
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Db 1531 TTTTAAATTAATTAATTAAT 1552

RESULT 15
US-10-295-027-1022
Sequence 1022, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295, 027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663, 733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350, 666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335, 394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332, 464
PRIOR FILING DATE: 2001-11-21
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PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347, 211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347, 349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355, 250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356, 714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 1022
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-1022

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGTCAAGCCGATGAGTCTCCCTGTGAGCCCAAGCCCTGAGCTCTCTGTGATCCCGGC 60
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Qy 1261 GCCCTGTTTTTGGCTCTTTTGTCTGTCAACAGGTCGGGTTCCTGTGTGAGATGAGA 1320
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 Qy 1441 GAGAGCGTAACTGTCTGTCTGTCTATGCACTTCTTTAACTGCAAGAAATT 1500
 Db 1471 GAGAGCGTAACTGTCTGTCTGTCTATGCACTTCTTTAACTGCAAGAAATT 1530
 Qy 1501 TTTTAAATTAATTTTAAAT 1522
 Db 1531 TTTTAAATTAATTTTAAAT 1552

Search completed: February 6, 2005, 07:34:55
 Job time : 866 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2005, 23:51:49 ; Search time 4444 Seconds
(without alignments)
12480.034 Million cell updates/sec

Title: US-09-967-237a-1

Perfect score: 1522

Sequence: 1 acagtcagccgcatgctcc.....ttaataataattataat 1522

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: gb_esc2:*
3: gb_hnc:*
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5: gb_esc4:*
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7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1467.4	96.4	1469	3	CR616345 full-length
4	1423.4	93.5	1492	3	CR590646 full-length
5	1024.8	67.3	1084	1	AL542336 full-length
6	920.8	60.5	1070	1	AL554705 full-length
7	903.4	59.4	1009	1	AL558378 full-length
8	891.4	58.6	916	5	BX423970 full-length
9	861.6	56.6	1071	1	AL554665 full-length
10	832	54.7	1017	5	BX401186 full-length
11	813.6	53.5	961	5	BX423969 full-length
12	797	52.4	971	7	CO579387 full-length
13	794.4	52.2	994	1	AL577748 full-length
14	789.4	51.9	1017	1	AL580216 full-length
15	772.6	50.8	927	1	AL555184 full-length
16	731.4	48.1	874	4	BC386425 full-length
17	669.8	44.0	689	6	CA425935 full-length
18	665.4	43.7	682	1	AI681707 full-length
19	665.4	43.7	836	5	BX383092 full-length
20	660.4	43.4	691	5	BX620600 full-length
21	650.6	42.7	795	2	AW083555 full-length
22	647	42.5	669	1	AI925646 full-length
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24	629.2	41.3	733	4	BG819731 full-length

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ALIGNMENTS

RESULT 1	CR597234	1541 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR597234	full-length cDNA clone CSOD1085YF18 of Placenta Cot 25-normalized			
DEFINITION	CR597234	of Homo sapiens (human).			
ACCESSION	CR597234.1	GI:50478041			
VERSION	CR597234.1	HTC; CDS; full-length			
KEYWORDS	HTC; CDS; full-length				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contract : Feng Liang Email : fliang@lifeitech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 1541)				
REFERENCE	Genoscope.				
AUTHORS	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :				
TITLE	BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr				
JOURNAL	- Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
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	/mol_type="mRNA"				
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	/release_type="Placenta Cot 25-normalized"				
	/plasmid="pCMVSPORT_6"				
ORIGIN	Query Match				
	99.2% Score 1510.4; DB 3; Length 1541;				
	Best Local Similarity 99.9%; Pred. No. 0;				
	Matches 1511; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	ACAGTCAGCCGATGCTCCCTGTGTCACGACCCCTGAGTCTCTGTGATTCGGGCC			
Db	30	ACAGTCAGCCGATGCTCCCTGTGTCACGACCCCTGAGTCTCTGTGATTCGGGCC			

QY 61 CCTGCTCCAGGCTCACTGTGCACTGTGCTCACTGTGCTTCTGATGCTGTCCAT 120
 DB 90 CCGTCTCCAGGCTCACTGTGCACTGTGCTGTGCTGTCTGCTTCTGTGCTGTCCAT 149
 QY 121 CCCCAAGGTTGCCCCGAGATGCAAGAGATTTCCCCCTTGGAGAGAGGCTCTTCTGGAGAA 180
 DB 150 CCCCAAGGTTGCCCCGAGATGCAAGAGATTTCCCCCTTGGAGAGAGGCTCTTCTGGAGAA 209
 QY 181 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 240
 DB 210 GATGACCACTGGGCGAGAGAGATCTGCCAGTGAAGAGATTTCAACCCAGAGAGAGAT 269
 QY 241 CCAACCCGAGAGAGAGATCTACTGTGAGAGAGATCTTCTGTGAGAGAGATCTTACTT 300
 DB 270 CCAACCCGAGAGAGAGATCTACTGTGAGAGAGATCTTCTGTGAGAGAGATCTTACTT 329
 QY 301 GAAGTTAAGCTTAATCAGAGAAGAGGCTCCCTGAAGTTAGAGATCTTACTTCTGTT 360
 DB 330 GAAGTTAAGCTTAATCAGAGAAGAGGCTCCCTGAAGTTAGAGATCTTACTTCTGTT 389
 QY 361 GAAGCTCTGTGAGATCTTCAAGAACCCAGAAATATGCCACAGAGGACAAAGAGAGAT 420
 DB 390 GAAGCTCTGTGAGATCTTCAAGAACCCAGAAATATGCCACAGAGGACAAAGAGAGAT 449
 QY 421 GACCAAGATCTATGGGCTTATGAGAGGACCCGCTGTGAGGCTGTGCTTCCAGGCTG 480
 DB 450 GACCAAGATCTATGGGCTTATGAGAGGACCCGCTGTGAGGCTGTGCTTCCAGGCTG 509
 QY 481 GCGGCGGCTTCAAGTCCCGGATGATCCGCGCCAGCTGCGGCTTCTGCGCGGCT 540
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 QY 601 AACATGCGCAAGTGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 630 AACATGCGCAAGTGTGCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
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 DB 690 GGGCGGAGTACCGGCTCTGTGAGCTGTGCACTGAGGAGGCTGAGGCTGCTGAG 749
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 DB 750 TCGGAGCACTGTGAGAGGCAACCGTTCCTGCGGAGATTCACGTGCTTCACTCAAC 809
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 QY 841 GCTTTCTGTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGAGCAGTGTGCTGCTG 900
 DB 870 GCTTTCTGTGAGAGAGGCGCCGAGAGAAACAGTGCCTATGAGCAGTGTGCTGCTG 929
 QY 901 GAGAAATGCTGTGAGAGAGGCTTCAAGACTCAGGTTCCAGAGCTGAGCAATCTGCACT 960
 DB 930 GAGAAATGCTGTGAGAGAGGCTTCAAGACTCAGGTTCCAGAGCTGAGCAATCTGCACT 989
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 DB 1050 GCCCAAGGATGATCTGAGCTGTGTTTAAACAGACAGTATGCTGAGTCTTAAAGAGCT 1109
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 DB 1110 CACACCTCTCTGAGACACCTGTGAGAGCTGTGACTCTTCCGCTTCAAGTGAATTTCCGA 1169

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 QY 1201 AGTCTCGGAGCTGTGAGCAGTCCAGCTGAATTCCTGAGCTGAGCTGTGAGTGAATCT 1260
 DB 1230 AGTCTCGGAGCTGTGAGCAGTCCAGCTGAATTCCTGAGCTGAGCTGTGAGTGAATCT 1289
 QY 1261 GCCCTGTTTTTGGCTCTCTTTTGTGCTGCAACAGCTGAGTTCCTTGTGAGATGAGA 1320
 DB 1290 GCCCTGTTTTTGGCTCTCTTTTGTGCTGCAACAGCTGAGTTCCTTGTGAGATGAGA 1349
 QY 1321 AGGCAACACAGAGGAGAACCAAGAGGCTGTGAGTACCGCCGAGAGAGTACCGAG 1380
 DB 1350 AGGCAACACAGAGGAGAACCAAGAGGCTGTGAGTACCGCCGAGAGAGTACCGAG 1409
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 DB 1410 ACTGAGCTTGAAGGCTGATCTTGAAGATGTGAGAGAGCAGCAGAGGATCTGAGAG 1469
 QY 1441 GAGCGGATTAATCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 DB 1470 GAGCGGATTAATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
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 DB 1530 TTTTAAATTA 1541

RESULT 2
 LOCUS CR620502 1523 bp mRNA linear HTC 21-JUL-2004
 DEFINITION Full-length cDNA clone CSODK007YK10 of Hela cells Cot 25-normalized
 of Homo sapiens (human).
 ACCESSION CR620502
 VERSION CR620502.1 GI:50501309
 KEYWORDS HTC; CNSLT; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1523)
 REFERENCE
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
 COMMENT
 - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NciI-oligo(dT) primer. Five primes
 into the Not I and BcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK007YK10"
 /tissue type="Hela cells Cot 25-normalized"
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ORIGIN

Query Match 98.7%; Score 1502.4; DB 3; Length 1523;
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 Matches 1503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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20 AAGGTGAGCGGATGCTCCCTGTGTCCTCCAGCCCTGTGCTCTGTGATCCCGGC 79
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80 CCGTCTCAGGCTCAGTGTGCACTGTGTGTGCTGTGCTGTGATGCTGTGCT 139
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140 CCCGAGGTTGGCCCGGATGAGAGGATTTCCCTTGGGAGGAGGCTCTTCTGGGAA 199
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200 GATGACCACTGGGCGAGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAT 259
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320 GAAGTTAAGCTTAATCAGAGAGAGGCTCCCTGAATTAAGAGATCTACTACTGTT 379
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380 GAGGCTCTGAGAGTCTCAAGAACCCAGAAATATGCCACAGGACAAAGAGAGGAT 439
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440 GACAGAGTCAATTTGGGCTATGAGAGGCGACCCGCTGTGGCCCGGATGCCAGCTGC 499
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500 GGGGGCGGCTTCAAGTCCCCGGTGAATATCCGCCCCAGTGTGCTGTGCTGTGCT 559
541 CTGGCCCCCTGGAATCTCTGGGCTTCAAGTCCCCGGTGTGCCAGAACTGGCCCTGC 600
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740 TCGAGACACACTGTGAGAGGCGACCGTTCCCTGCGAGATCCAGTGTGCTGCTGAC 799
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1160 GCGCAGGGGTGCTATCTGAGCTGTGTTTAAACAGACAGTGTGAGTGTGCTAAGCAGCTC 1219
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1400 ACTGAGCTTGAAGGCTGTGATCTTGAAGATGTGAAGCCAGCCAGAGGATCTGAGGG 1459
1441 GGAGCGGTAACTGTCTGTCTGTCTCATTAATGCACTTCTTTAACTGCCAAGAAAT 1500
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1501 TTTT 1504
1520 TTTT 1523

RESULT 3

LOCUS

CR616345 1469 bp mRNA linear HTC 21-UTL-2004

DEFINITION

full-length cDNA clone CS0DA003YB12 of Neuroblastoma of Homo sapiens (human).

ACCESSION

CR616345.1 GI:50497152

VERSION

HTC; CINSUT_cDNA.

KEYWORDS

Source

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1469)

AUTHORS

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 1469)

REFERENCE

Genoscope.

AUTHORS

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : segre@genoscope.cns.fr

TITLE

- Web : www.genoscope.cns.fr)

JOURNAL

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen

FEATURES

Location/Qualifiers

1..1469

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="CS0DA003YB12"

/tissue_type="Neuroblastoma"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match

96.4%; Score 1467.4; DB 3; Length 1469;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1468; Conservative 0; Mismatches 1; Indels 0; Gaps 0

OY	9	CCGCAATGAGTCCCTGTGCGCCAGCCCTGGCTCCCTCTGTGATCCCGGCCCTGTCC	68
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Db	61	AGGCTCACTGTGCACTGTGTGTGATCACTGTGCTTCTGATGTCTTCATCCCAAG	120
OY	129	GTTGCCCGGATGCAAGAGATTCCCCCTTGGAGAGAGCTCTTCTGGGGAAGATGACC	188
Db	121	GTTGCCCGGATGCAAGAGATTCCCCCTTGGAGAGAGCTCTTCTGGGGAAGATGACC	180
OY	189	ACTGGGCGAAGAGATCTGCCCACTGAGAGAGATTCAACCAGAGAGAGATCAACCCGG	248
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OY	309	GCTTAATCAGAAAGAGAGGCTCCCTGAAAGTTAAGATCTACCTAGTTGAGGCTCC	368
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OY	609	CCAAGTGTGCACTGACCTGTGCTTCTGGGCTAAGATGGCTCTGGGTCCCGGCGGGA	668
Db	601	CCAAGTGTGCACTGACCTGTGCTTCTGGGCTAAGATGGCTCTGGGTCCCGGCGGGA	660
OY	669	GTAACGGGCTCTGAGCTGCACTGTGCACTGGGGGGGTGAGAGTGTCCGGGCTCGAGCA	728
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Db	721	CACGTGAAAGGCCACCGCTTCCCTGCGGAGATCAAGTGGTTCACTTCAGCAGCGCTT	780
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OY	969	TGACTTCAAGCGCTACTTCAATATAGAGGGGTCTGTGACTACCGGCTGTGCCAGG	1028
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Query Match	93.5%	Score 1423.4	DB 3	Length 1492
ORIGIN				
Query Match	93.5%	Score 1423.4	DB 3	Length 1492


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DB 330 GAAAGTTAAAGCTTAATCAGAGAGAGAGGCTCCCTGAAAGTAGAGANTCTACTACTGT 389
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DB 570 CTGCGCGCGCTTCAAGTCCCGGATGATATCCGCGCGCTGCGCGCTTCTGCGCGGCG 629
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QY 1020 TGCCCAAG 1027
DB 1042 TGCCCAAG 1049

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RESULT 7
AL558378 1009 bp mRNA linear EST 02-APR-2004
DEFINITION AL558378 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION AL558378
VERSION AL558378.3 GI:46183776
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1009)
AUTHORS Li W.B., Gruber C., Jessee J. and Polyes J.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31280177.
Contact: Genome
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

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ORIGIN

Query Match 59.4%; Score 903.4; DB 1; Length 1009;
 Best Local Similarity 99.1%; Pred. No. 1.8e-216;
 Matches 956; Conservative 4; Mismatches 0; Indels 5; Gaps 5;

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 571 CTGCGCGCGCTTCAAGTCCCGGATGATATCCGCGCGCTGCGCGCTTCTGCGCGGCG 630
 601 AACCAATGGCCACAGTGTGCAACTGACACCTGCTCTGAGGCTAGAGATGAGTCTGAGTCCC 660
 631 AACCAATGGCCACAGTGTGCAACTGACACCTGCTCTGAGGCTAGAGATGAGTCTGAGTCCC 690

FEATURES

source

Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5300.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna7as=CS0D0J05BF07QPlac=5300.f.
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 /clone="CS0D0J05YK14"
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 /clone_1ib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

QY 661 GGGCGGAGATACCGGCTCTGACGCTGCACTGCGGGGGGCTGCAAGGTGTCGCGGC 720
Db 691 GGGCGGAGATACCGGCTCTGACGCTGCACTGCGGGGGGCTGCAAGGTGTCGCGGC 750
QY 721 TCGAGACACATCTGAGAGAGCCAGCTTCCCTGCGAGATCAGCTGCTTCACTCAGC 780
Db 751 TCGAGACACATCTGAGAGAGCCAGCTTCCCTGCGAGATCAGCTGCTTCACTCAGC 810
QY 781 ACCGCTTTTGGCAGAGTTGACGAGGCTTGGGGGCGCGGAGAGGCTGCGCTGTTGGC 840
Db 811 ACCGCTTTTGGCAGAGTTGACGAGGCTTGGGGGCGCGGAGAGGCTGCGCTGTTGGC 869
QY 841 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATAGACAGTGTGCTGCTGG 900
Db 870 GCGTTTCTGAGAGAGGCGCGGAGAGAAACAGTGCCTATAGACAGTGTGCTGCTGG 928
QY 901 GAAAGAAATCGTGAAGAGGCTCAGAGACTCAGAGTCCAGAGCTGAGACATATCTGACTC 960
Db 929 GAA-RAATGCTGAGGAA-GCTCAGAGACTCAGAGKCCAGAGCTGAGACAMAT-TGCACTC 985
QY 961 CTGCC 965
Db 986 CTGCC 990

RESULT 8
LOCUS BX423970 916 bp mRNA linear EST 03-MAY-2004
DEFINITION BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CS00A003YB12 5-PRIME, mRNA sequence.
ACCESSION BX423970
VERSION BX423970.2 GI:46955310
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30766328.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by life technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSIDA001ZF09qPlc=5300.f.

FEATURES
source
1. 916
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS00A003YB12"
/issue_type="NEUROBLASTOMA"
/clone_id="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 58.6%; Score 891.4; DB 5; Length 916;
Best Local Similarity 96.4%; Pred. No. 1.9e-213;
Matches 883; Conservative 23; Mismatches 10; Indels 0; Gaps 0;

QY 9 CGGATGGCTCCCGTGGTCCCGGAGCCCTGGGCTCCCTGTTGATCCCGGCGCTGCTCC 68
Db 1 CGGATGGCTCCCGTGGTCCCGGAGCCCTGGGCTCCCTGTTGATCCCGGCGCTGCTCC 60
QY 69 AGGCTCACTGTCGCAACTGCTGCTGCTCACTGCTGCTTGTGATGCTGTCATCCCAAG 128
Db 61 AGGCTCACTGTCGCAACTGCTGCTGCTCACTGCTGCTTGTGATGCTGTCATCCCAAG 120
QY 129 GTTCCCGCGGATTCGAGAGATTTCCCTTTGGAGAGAGGCTCTTTGGGAAAGATGACC 188
Db 121 GTTCCCGCGGATTCGAGAGATTTCCCTTTGGAGAGAGGCTCTTTGGGAAAGATGACC 180
QY 189 ACTGGGCGAGAGAGATTCGCCAAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGG 248
Db 181 ACTGGGCGAGAGAGATTCGCCAAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGG 240
QY 249 AGAGAGAGATTCCTGAGAGAGAGATTCCTGAGAGAGAGATTCCTGAGAGATTCCTGAG 308
Db 241 AGAGAGAGATTCCTGAGAGAGAGATTCCTGAGAGAGAGATTCCTGAGAGATTCCTGAG 300
QY 309 GCTTAATCAGAAAGAGGCTCCCTGAAGTGAAGATTCCTGAGAGATTCCTGAGAGATTC 368
Db 301 GCTTAATCAGAAAGAGGCTCCCTGAAGTGAAGATTCCTGAGAGATTCCTGAGAGATTC 360
QY 369 TGGAGATCCTCAAGAACCCAGAAATATGATCCCAAGAGCAAGAAAGAGATGACCAAG 428
Db 361 TGGAGATCCTCAAGAACCCAGAAATATGATGATCCCAAGAGCAAGAAAGAGATGACCAAG 420
QY 429 TCATTGGGCTATGAGAGGAGACCGGCTCTGGAGGCTGCTCCAGGCTGCGGAGGCGG 488
Db 421 TCATTGGGCTATGAGAGGAGACCGGCTCTGGAGGCTGCTCCAGGCTGCGGAGGCGG 480
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Db 481 CTTCAGATCCCGGCTGATATCCGCGCCAGCTGCGGCTCTTTCGCGGCTCTGCGGCTCC 540
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QY 609 CCACAGTGTGCAACTGACCTGCTCTGAGGCTGAGATGCTGAGTCCCGGCGGAG 668
Db 601 CCACAGTGTGCAACTGACCTGCTCTGAGGCTGAGATGCTGAGTCCCGGCGGAG 660
QY 669 GTACCGGCTGTGACGCTGCACTTGCATTTGGGGGCTGCAAGTCTCCGGGCTCGAGGA 728
Db 661 GTACCGGCTGTGACGCTGCACTTGCATTTGGGGGCTGCAAGTCTCCGGGCTCGAGGA 720
QY 729 CACTGTGAAGGCGACCGTTCCCTGCGGAGATCCACGAGTTCACCTGAGACCGCTT 788
Db 721 CACTGTGAAGGCGACCGTTCCCTGCGGAGATCCACGAGTTCACCTGAGACCGCTT 780
QY 789 TGCAGAGTTGACGAGGCTTGGGGGCGCGGAGAGGCTGCGGCTGTTGGCGGCTTCT 848
Db 781 TGCAGAGTTGACGAGGCTTGGGGGCGCGGAGAGGCTGCGGCTGTTGGCGGCTTCT 840
QY 849 GAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGAGATTTGCTGCTGCTGAGAAAT 908
Db 841 GAGAGAGGCGCGGAGAGAAACAGTGCCTATGAGAGATTTGCTGCTGCTGAGAAAT 900
QY 909 CGCTGAGAGAGGCTCA 924
Db 901 MCTGAGAGAGGCTCA 916

RESULT 9
LOCUS AL554665/1 1071 bp mRNA linear EST 30-MAR-2004
DEFINITION AL554665 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS00I085YF18 3-PRIME, mRNA sequence.
ACCESSION AL554665
VERSION AL554665.3 GI:45859416
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eularchia: Primates: Catarrhini, Homnidae, Homo. 1 (bases 1 to 1071)
AUTHORS	Id,M.B., Gruber,C., Jeasee,J. and Polayres,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31276475.

Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segeret@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five primase
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0D1085DC09NP1&c=5300.f>.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSOD10851F18"
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/notes="1st strand cDNA was primed with a NotI-oligo (nr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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ORIGIN

Query Match	56.6%	Score	861.6	DB 1	Length	1071
Best Local Similarity	93.6%	Pred	No. 6.4e-206			
Matches 1003	Conservative	21	Mismatches	31	Indels	17
					Gaps	12

QY 451 CGGCGCTGAGGCCGGAGTGTCCCAAGCTACGGGGGCGCTTCCAGTACCCCGAGGATATC 510

Db 1066 CGCGCCTTGTGSCCAGSAGTGTCCCAAGCTACGCG- GAGCGGCTHMAATGCCCGAT- GATATC 100

QY 511 CGCGCCCAAGCTGCGCGCTTCTGCGCGAGCCCTGCGGCCCTGAGAACTCGTGGGCTTCCAG 570

Db 1008 CGCGCCCGAG- TFGCGCGCTTGTGCCCG- CTVGGCGCCCTTGA-- CTCCTGASTTCCVG 953

QY 571 CTCGCGCGGCTTCCCAAGACTGGGCTTGGCGAACAATGGCCACAGTGTGCACTGACCCTG 630

Db 952 STCCCSGCGCTCCCAAGACTGCG- CTGCCCAACAATGGCCACAGTGTGCAACTGACCCCTG 894

QY 631 CCTCGTGGAGTAGAATATGGCTCTGGGGTCCCGGGCGGGAATACCGGGCTGTGACAGCTGCAT 690

Db 893 CCTCTGGAGTAGAATATGGCTCTGGGGTCCCGGGCGGGAATACCGGGCTGTGACAGCTGCAT 834

QY 691 CTGCACTGGGGGCTGCAAGTGTCTCGAGGCTCGAGACACTGTGGAAGGCCACCGTTTC 750

Db 833 CTGMACTGGGGGCTGCAAGTGTCTCGAGGCTCGARCACACTGTGGAAGGCCACCGTTTC 774

QY 751 CCTGCGGAGATTCACGTGTTCACCTCAGACCGGCTTTTGCAGAGTTGACGAGGCGTTG 810

Db 773 CCTGCGGAGATTCACGTGTTCACCTCAGACCGGCTTTTGCAGAGTTGACGAGGCGTTG 714

QY 811 GGGGCGCCGGGAGGCGCTGGCGGTGGCGGCTTTCTGAGAGAGGCGCCGGAAGAAAAC 870

Db 713 GGGGCGCCGGGAGGCGCTGGCGGTGGCGGCTTTCTGAGAGAGGCGCCGGAAGAAAAC 654

QY 871 AGTGCCTATGAGCAGTGTCTGTCTCGCTTGGAGAAATCGCTGAGGAGGCTCAGAGACT 930

Db 653 AGTGCCTATGAGCAGTGTCTGTCTGCTTGGAGAAATCGCTGAGGAGGCTCAGAGACT 594

QY 931 CAGGTCCAGGACT--GGAACATATGTGCACTCTCT- GCCTCTGACTTTCAGCG- CTACTT 986

Db	593	CAGGTCCAGACATCGGACATCTCTGACTCTCCGCCCTCTCACTTCAGCGCCCACTT	534
QY	987	CCAAATATGAGGGGGTCTCTGACTAACCGGCCCTGTGGCCAGGGTGTCACTCTGGACTGTGT	1046
Db	533	CCAAATATGAGGGGGTCTCTGACTAACCGGCCCTGTGGCCAGGGTGTCACTCTGGACTGTGT	474
QY	1047	TAACCAAGCAGTATGCTGAGTGTCTAAGACAGCTCCACCCCTCTGTGACACCTGTGGGG	1106
Db	473	TAACCAAGCAGTATGCTGAGTGTCTAAGACAGCTCCACCCCTCTGTGACACCTGTGGGG	414
QY	1107	ACCTGTGACTCTGTGGCTACAGCTGAATCTTCAGACGACGACGACCTTTGATGGGCGAGT	1166
Db	413	ACCTGTGATCTCTGGCTACAGCTGAATCTTCAGACGACGACGACCTTTGATGGGCGAGT	354
QY	1167	GATTGAGGCTCTTTCCTCTGTGTGAGTGACAGCAGTCTCTGGGCTGTGAGCCAGTCCA	1226
Db	353	GATTGAGGCTCTTTCCTCTGTGTGAGTGACAGCAGTCTCTGGGCTGTGAGCCAGTCCA	294
QY	1227	GCTGAATTCCTCTGCTGGCTGTGTGTGACATCTTAGCCCTTGTTTTTGGCCCTCTTTTTC	1286
Db	293	GCTGAATTCCTCTGCTGGCTGTGTGTGACATCTTAGCCCTTGTTTTTGGCCCTCTTTTTC	234
QY	1287	TGTGACCAAGCGTGTGCTTCTCTGTGCAATGAGAAAGGACAGACAGAAAGGGGAAACCAAG	1346
Db	233	TGTGACCAAGCGTGTGCTTCTCTGTGCAATGAGAAAGGACAGACAGAAAGGGGAAACCAAG	174
QY	1347	GGGTGTGAGCTAACCGCCACGACAGAGTAAAGCCGAACTGTAGC--CTAGAGCTGTGATCT	1403
Db	173	GGGTGTGAGCTAACCGCCACGACAGAGTAAAGCCGAACTGTAGACCTAAGACGACATGAGATCT	114
QY	1404	TGAGAAATGTGAGAAAG--CCAGCCAGAGGCACTTGAAGGGGGAGCCGGTAACTGTCTGTCTC	1461
Db	113	TGAGAAATGTGAGAAAGACACAGCCAGAGGCACTTGAAGGGGGAGCCGGTAACTGTCTGTCTC	54
QY	1462	CTGCTCATATATAG--CCACTTCCTTTTAATCTGCAAGAAATTTTAAATAATAA	1512
Db	53	CTGCTCATATATAGCCACTCTCTTTTAACTGCAAAANNNVVTTTTTAAATAA	2

RESULT 10

LOCUS	BX401186	1017 bp	mRNA	linear	EST 29-APR-2004
DEFINITION	BX401186 Homo sapiens HELA CELLS COR 25-NORMALIZED Homo sapiens				
	cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.				
ACCESSION	BX401186				
VERSION	BX401186.2	GI:46876709			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1, (bases 1 to 1017)
L.J.W.B., Gruber,C., Jesse,J. and Poljacek,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30626393

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.F

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?v=CS0DK09DHDH05QPI&c=5300.F>

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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 54.7%; Score 832; DB 5; Length 1017;
Best Local Similarity 97.4%; Pred. No. 1.8e-198;
Matches 896; Conservative 3; Mismatches 13; Indels 8; Gaps 5;

1 ACAGTACGCGGATGCTCCCTGTCGCGCCAGCCCTGCTCTCTGTGATCCCGGCC 60
2 ACAGTACGCGGATGCTCCCTGTCGCGCCAGCCCTGCTCTCTGTGATCCCGGCC 60
61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGTCACTGTGCTGTGCTGTGCTGTGCT 120
61 CCTGCTCCAGGCTCACTGTGCACTGTGCTGTCACTGTGCTGTGCTGTGCTGTGCT 120
121 CCCCAAGAGTGTGCTCCCGATGCAAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAA 180
121 CCCCAAGAGTGTGCTCCCGATGCAAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAA 180
181 GATGACCCCACTGGGCGAGAGAGATCTGCCCACTGAAGAGATTTCAACCCAGAGAGAGAT 240
181 GATGACCCCACTGGGCGAGAGAGATCTGCCCACTGAAGAGATTTCAACCCAGAGAGAGAT 240
241 CCACCCGAGAGAGAGATTTACCTGAGAGAGAGATTTACCTGAGAGAGAGATTTACT 300
241 CCACCCGAGAGAGAGATTTACCTGAGAGAGAGATTTACCTGAGAGAGAGATTTACT 300
301 GAAGTTAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTGAAGATTTACTTCTGT 360
301 GAAGTTAAGCTTAATCAAGAAAGAGGCTCCCTGAAGTGAAGATTTACTTCTGT 360
361 GAGGCTCTGAGAGATTTCTCAAGAACCCCAAGATTAATGCCCAAGAGAGAGAGAT 420
361 GAGGCTCTGAGAGATTTCTCAAGAACCCCAAGATTAATGCCCAAGAGAGAGAGAT 420
421 GACCAAGATTTGCGGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
421 GACCAAGATTTGCGGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
481 GCGGCGCGGCTTCAAGTCCCGGTGATATCCGCCCCCAGCTGCGCGCTTCTGCGCGCC 540
481 GCGGCGCGGCTTCAAGTCCCGGTGATATCCGCCCCCAGCTGCGCGCTTCTGCGCGCC 540
541 CTGCGCGCGCTTGAACCTCTGAGGCTTCCAGCTCCGCGCGCTTCCAGAACTGCGCTGCGC 600
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601 AACCAATGCAAGATTTGCACTGACCTGCTCTGAGGCTGAGAGAGAGAGAGAGAGAG 660
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781 ACCGCTTTGCAAGATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 ACCGCTTTGCAAGATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 GCGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 GCGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
893 GCGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893

QY 901 GAGAAATTCCTGAGAGAG 920
DB 894 GAGAAATTCCTGAGAGAG 913

RESULT 11
BX423969/c 961 bp mRNA linear EST 03-MAY-2004
LOCUS BX423969 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CSODA003YB12 3-PRIME, mRNA sequence.
ACCESSION BX423969
VERSION BX423969.2 GI:46954391
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 961)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi.3076327.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna7s-CSIDA001ZF09NP1&c=5300.f.

FEATURES

source
1..961
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA003YB12"
/issue_type="NEUROBLASTOMA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 53.5%; Score 813.6; DB 5; Length 961;
Best Local Similarity 89.7%; Pred. No. 7.9e-194;
Matches 852; Conservative 24; Mismatches 71; Indels 3; Gaps 2;

513 CCCCAGTCCGCGGCTTCTGCGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 572
513 CCCCAGTCCGCGGCTTCTGCGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 572
DB 961 CCCCCCGGCTGCGGCTTCTGCGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 904
961 CCCCCCGGCTGCGGCTTCTGCGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT 904
QY 573 CCGGCGGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACT 632
573 CCGGCGGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACT 632
DB 903 CCGGCGGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACT 845
903 CCGGCGGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACTGCGCTTCCAGAACT 845
QY 633 TCTGAGGCTTAAGATGCTTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 692
633 TCTGAGGCTTAAGATGCTTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 692
DB 844 TCTGAGGCTTAAGATGCTTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 785
844 TCTGAGGCTTAAGATGCTTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 785
QY 693 GCACTGGGCGGCTGAGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 752
693 GCACTGGGCGGCTGAGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 752
DB 784 GAACTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 725
784 GAACTGGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCTTCCGCGGCT 725
QY 753 TCCGAGATTCAGGCTTCCAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 812
753 TCCGAGATTCAGGCTTCCAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 812
DB 724 TCCGAGATTCAGGCTTCCAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 665
724 TCCGAGATTCAGGCTTCCAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 665


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QY      813 GGGCCGGGAGGCGCTGGCCGCTGGGCGCCCTTTCTGAGAGAGGGCCGGAAGAAAACAG 872
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QY      873 TGCCTATGAGCAGATTGCTGTCTCGCTGGAGAAAATCGCTGAGAGAGGCTCAGAGACTCA 932
DB      604 TGCCTATGAGAGAGTGTCTGTCTCGCTGGAGAAAATCGCTGAGAGAGGCTCAGAGACTCA 545
QY      933 GGTCCAGAGAGCTGAGACATATCTGCACTCTGCTCCCTCTGACTTCAAGCCGCTACTTCCAAAT 992
DB      544 GGTCCAGAGAGCTGAGACATATCTGCACTCTGCTCCCTCTGACTTCAAGCCGCTACTTCCAAAT 485
QY      993 TGAAGGGGCTCTGACTGACACAGCCGCTGTGGCCAGGGGTGCATCTGAGACGTGTAAACCA 1052
DB      484 TGAAGGGGCTCTGACTGACACAGCCGCTGTGGCCAGGGGTGCATCTGAGACGTGTAAACCA 425
QY      1053 GACAGTGTATGCTGATGCTTAAAGCTTCAACACCTCTCTGACACCTGTGTGGGAGACTGG 1112
DB      424 AACAGTGTATGCTTAAAGCTTCAACACCTCTCTGACACCTGTGTGGGAGACTGG 365
QY      1113 TGACTCTGGGCTTACAGCTGAACTTCCAGAGCAGAGCCTTTGGAATGGGCTGAGTATGA 1172
DB      364 TAACTCTGGGCTTACAGCTGAACTTCCAGAGCAGAGCCTTTGGAATGGGCTGAGTATGA 305
QY      1173 GGGCCCTCTTCCCTGGCTGAGAGAGAGAGCTGCTGGGCTGTGAGCCAGTCCAGCTGAA 1232
DB      304 GGGCCCTCTTCCCTGGCTGAGAGAGAGAGCTGCTGGGCTGTGAGCCAGTCCAGCTGAA 245
QY      1233 TTCTGCTGCTGCTGCTGTGATGATCTTACCTTACCTTGTGCTTCTTCTTCTGCTGCTAC 1292
DB      244 TMCCTGCTGCTGCTGCTGTGATGATCTTACCTTACCTTGTGCTTCTTCTTCTGCTGCTAC 185
QY      1293 CAGCGTCCGCTTCTTGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
DB      184 CAGCGTCCGCTTCTTGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
QY      1353 GAGCTACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1412
DB      124 GAGCTACCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 65
QY      1413 TGAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1462
DB      64 TGAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 15

RESULT 12
COS79387 971 bp mRNA linear EST 20-JUL-2004
LOCUS DEFINITION ILLUMISEN_MCO_50239 Katze_MML Macaca mulatta cDNA clone
IBIW:17608 5' similar to Bases 6 to 971 highly similar to human
CA9 (Hb.63287), mRNA sequence.
COS79387
COS79387.1 GI:50410317
EST:
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 971)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.
Michael Katze lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see

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http://www.macaque.org
PCR Primers
FORWARD: CCTCCTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGCTA
Insert Length: 971 Std Error: 0.00
Plate: CL000413 row: A column: 10
Seq primer: CCTCCTAAAGGGAACAAA
POLYA=No.

FEATURES
source
location/Qualifiers
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/mol_type="mRNA"
/strain="Indian"
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/lab_host="Electromax DH10B"
/clone_1ib="Katze_MML"
/note="Organ: ileum; Vector: pDONR 222; Site 1: Bsrc 1;
Site 2: Bsrc 1; Created from Cloneminer cDNA Library
Construction kit (catalog #18249-029)"

ORIGIN
Query Match 52.4%; Score 797; DB 7; Length 971;
Best Local Similarity 93.0%; Pred. No. 1.2e-189;
Matches 890; Conservative 0; Mismatches 60; Indels 7; Gaps 5;

212 GTTAAAGAGATTACCCAGAGAGAGAGATTCACCCGAGAGAGAGATCTTACTGAGAGG 271
DB 4 GGGAGAGATGACCACTGATGAGAGAGATCTGCCAGTGAAGAGATCCACCAAGAGG 63
QY 272 AGGATCTACCTGAGAGAGAGATCTTAAAGTTAAAGCTTAAATCAAGAGAGAGGCT 331
DB 64 AGGATCTACCCAGAGAGAGAGATCTTAAAGTTAAAGCTTAAATCAAGAGAGAGGCT 123
QY 332 CCTGAAGTTAGAGATCTTAAAGTTAGAGGCTCTGAGAGATCTCAAGAACCCAGAG 391
DB 124 CCTGAAGTTAGAGATCTTAAAGTTAGAGGCTCTGAGAGATCTCAAGAACCCAGAG 183
QY 392 ATTAATGCCACAGGAGCAAGAGAGAGATGACAGAGTCAATTGGGCTATGAGGCGAGC 451
DB 184 ATTAATGCCACAGGAGCAAGAGAGAGATGACAGAGTCAATTGGGCTATGAGGCGAGC 243
QY 452 CGCCCTGGCCCGGAGTGTCCCAAGCTGCGCGGCGCGCTTCCAGTCCCGGCTGATATCC 511
DB 244 CGCCCTGGCCCGGAGTGTCCCAAGCTGCGCGGCGCGCTTCCAGTCCCGGCTGATATCC 303
QY 512 GCCCCAGCTGCGGCTTCTGCGCCGCGGCGGCGGCGGCTGGAATCTCGGAGCTTCCAGC 571
DB 304 GCCCCAGCTGCGGCTTCTGCGCCGCGGCGGCGGCGGCTGGAATCTCGGAGCTTCCAGC 363
QY 572 TCCCGCGCTCCAGAACTGCGCTGCGCAACATGAGCCACAGTGTGCAACTGACCTTGC 631
DB 364 TCCCGCTGCTCCAGAACTGCGCTGCGCAACATGAGCCACAGTGTGCAACTGACCTTGC 423
QY 632 CTCCTGGGCTAGAGATGCTCTGGGTTCCCGGCGGAGATACCGGCTCTGCACTGATC 691
DB 424 CTCCTGGGCTAGAGATGCTCTGGGTTCCCGGCGGAGATACCGGCTCTGCACTGATC 483
QY 692 TGCACCTGGGGGCTGACAGGTGTGCGGGCTGGAGACACATGTGAGAGGCCACCGTTCC 751
DB 484 TGCACCTGGGGGCTGACAGGTGTGCGGGCTGGAGACACATGTGAGAGGCCACCGTTCC 543
QY 752 CTGCGAGATCCAGCTGTGTTCACTCAGACCGCTTTTCCAGAGTTGACAGAGGCTTGG 811
DB 544 CTGCGAGATCCAGCTGTGTTCACTCAGACCGCTTTTCCAGAGTTGACAGAGGCTTGG 603
QY 812 GGGCG-CCGGGAGGCTTGGCGGTGTTGGCCGCTTTCTGAGAGAGGCGCCGGAAGAAC 870
DB 604 GGGCGCCCGGAGGCGCTGGCGGTGTTGGCCGCTTTCTGAGAGAGGCGCCGGAAGAAC 663
QY 871 AGTGCCTATGAGCACTTGTCTGCTTGGAGAGAAATCGCTGAGAGAGGCTCAGAGACT 930

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Db	664	AGTGCCTATGAGCAGTTGCTGTCTCACTTGGAGAAATTCGCTGAGGAAGGCTCAGAGACT	723
Qy	931	CAGGTCCCAAGGACCTGGACATATCTGCACTCCGCGCTGATCTTCAAGCGGTAATTCCAA	990
Db	724	CAGTCCCAAGGACTGGACGTAATCTGCACTCTCGCGCTGACCTGAGCGGTAATTCTCGA	783
Qy	991	TATGAGGGGCTCTGTGACTTACACCGCGCTGTGCGCCAGGGTGTATCT--GAGCTGTGTTTAA	1049
Db	784	TATGAGGGGCTCTGTGACTTACACGCGCTGTGCGCGGCTGTGATCTTGGAGACTGTGTTTAA	843
Qy	1050	CCAGACAGTGTGCTGAGTGCCTAAGCAGACTCCACACCTCTCTGTGACACCT--GTGGGGAC	1108
Db	844	CCAGACAGTGTGCTGAGTGCCTAAGCAGACTCCACACCTCTCTGTGAGGCTGTGGGGGGAC	903
Qy	1109	CTGGTGAATCT--CGGCTACAGCTGAATCTTC---GAGGAGCGCACTTTTGAATGGG	1161
Db	904	CTGGGGATCTTCCCGGCTACGGCTGAATCTTCCGAAGGGAGCCACCTCTTGAATATGGG	960

RESULT 13	
AL577748/c	
LOCUS	AL577748 994 bp mRNA linear EST 07-APR-2004
DEFINITION	AL577748 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
ACCESSION	CDNA clone CS0DK007YK10 3-PRIME, mRNA sequence.
VERSION	AL577748
KEYWORDS	AL577748.3 GI:46256749
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	1 (bases 1 to 994)
AUTHORS	Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 16, 2001 this sequence replaced gi:31316001.

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
The first strand cDNA was primed with a NotI-oligo (dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 5300.F
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?ts=CS0DXK07BPF05NP1&c=5300.F>.
T. Chirion/Dovilsky

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SOURCE
1. .994
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_id="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-cligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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Query Match	52.2%	Score 794.4	DB 1	Length 994
Best Local Similarity	86.3%	Fred. No. 5.5e-189		
Matches 852	Conservative	46	Mismatches 84	Indels 5
				Gaps 4
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Db	985	TCGCGCCCGCTCCCGCTCTTATGCGCCGCTCTCCCGGAAATCTCTGAGTCTCCGCTCCCGC	926	
QY	581	TCGCGAAGCTCGCGCTGCGCAACAATGCGCACAATGTGTCAACTGACCTCGCTCTCTGCGC	640	

Db	925	CTYCCGAGVACTCTCCTCTCKGMACAAKGCGCAAC - KGTGMAATGMCCTTSCYCGYKGGGC	867
Qy	641	TAAGATGGCTCTYGGGTCCCGGGCGGGAGTACCGGGCTCTGCAGCTGCATCT - GCACTGG	699
Db	866	KAGGAATGGCTCTGGGTCCCGGGCGGGAGTACCGGGCTCTGCAGGTCTMTSTYGCACKGG	807
Qy	700	GGGACTCAGGTGCTCCGGGCTCGAGACACTGTGGAAAGCCACCGTTCCTGCGCGAG	759
Db	806	GANCTCAGGAKGCTCCKGGSTCGAGACATGGGGGAGAGCCACCGGTCCCGCGGAG	747
Qy	760	ATCCAGTGGTCACTCTCAGCACTGGCTTTGCCAGTGTACGAGGCTTGGGCGCGCG	819
Db	746	ATCCAGGGGTAKCACTCAGCACCGCTTTGCCAGTGTACGAGGCT - TKGGGCGCGCG	688
Qy	820	GGAGCGCTGGCCGTTTGGCGCGCTTCTGGAAGAGGCGCCGGAGAAACAGTGGCTAT	879
Db	687	GGAGCCCTGGCCGTTTGGCGCGCTTCTGGAAGAGGCGCCGGAGAAACAGGCTAT	628
Qy	880	GAGCAGTGTGCTCTCGCTTGGAAAGAAATGCTGAGAGAGGCTCAGAGCTCAGGTCCA	939
Db	627	GAGCAGTGTGCTCTCGCTTGGAAAGAAATGCTGAGAGAGGCTCAGAGCTCAGGTCCA	568
Qy	940	GGAATGCAATATTTGACATCTCTGCTCTCTGACTTTCAGCCGCTATCTCCAAATAGAGGG	999
Db	567	GNACTGCAATATTTGACATCTCTGCTCTCTGACTTTCAGCCGCTATCTCCAAATAGAGGG	508
Qy	1000	TCTGTACTACACCGCCCTGTGCCAGGGGTGATCATCGACTGTGTTTAAACAGACAGTG	1059
Db	507	TCTGTACTACACCGCCCTGTGCCAGGGGTGATCATCGACTGTGTTTAAACAGACAGTG	448
Qy	1060	ATGCTGAGTCTAAGCAGCTTCCAACCCCTCTGTGACACCCGTGGGGACCTGTGACTCT	1119
Db	447	ATGCTGAGTCTAAGCAGCTTCCAACCCCTCTGTGACACCCGTGGGGACCTGTGACTCT	388
Qy	1120	CGGCTCAGCTGAACTTCCGAGGGAGCGACCCCTTGAATGGGGAGATTTGAGGCTCC	1179
Db	387	CGGCTCAGCTGAACTTCCGAGGGAGCGACCCCTTGAATGGGGAGATTTGAGGCTCC	328
Qy	1180	TTCCCTGCTGGAAGTGAACAGCAGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGC	1239
Db	327	TTCCCTGCTGGAATTTGSAACAGCAGTCTCGGGCTGTGAGCCATTCAGCTGAATTCCTGC	268
Qy	1240	CTGGCTCTCTGTGACATCTCTAGCCCTGTGTTTGGCTCCTTTTGTGTACACAGGTC	1299
Db	267	CTGGCTCTCTGTGACATCTCTAGCCCTGTGTTTGGCTCCTTTTGTGTACACAGGTC	208
Qy	1300	GCCTTCTTGTGACATGATGAAGAGCAGACAGAAAGGGAAACAAAGGGGTGTGAGCTAC	1359
Db	207	GCCTTCTTGTGACATGATGAAGAGCAGACAGAAAGGGAAACAAAGGGGTGTGAGCTAC	148
Qy	1360	CGCCACAGAGGTAGGCTCGAGACTGAGACCTTAAGGCTGTGATTTGGAGATGTGAGAG	1419
Db	147	CGCCACAGAGGTAGGCTCGAGACTGAGACCTTAAGGCTGTGATTTGGAGATGTGAGAG	88
Qy	1420	CGAGCCAGAGCAATCTGAGGGGAGCGCGTAACTGTCTCTGTGCTCATTTAGCCA - C	1477
Db	87	CGAGCCAGAGCAATCTGAGGGGAGCGCGTAACTGTCTGTGCTCATTTAGCCA - C	28
Qy	1478	TTCTCTTAACTGCAAGAAATTTTTT	1504
Db	27	TTCTCTTAACTGCAAGAAATTTTTT	1

RESULT	14
AL580216/c	
LOCUS	1017 bp mRNA linear EST 07-APR-2004
DEFINITION	AL580216 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION	Homo sapiens cDNA clone CS0D005YK14 3-PRIME, mRNA sequence.
VERSION	AL580216
KEYWORDS	AL580216.2 GI:31318495
SOURCE	EST.
	Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1. (bases 1 to 1017)
AUTHORS
L.I. W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 16, 2001 this sequence version replaced gi:12946023.

ORIGIN

Query Match 51.9%; Score 789.4; DB 1; Length 1017;
Best Local Similarity 87.9%; Pred. No. 1e-187;
Matches 832; Conservative 44; Mismatches 66; Indels 4; Gaps 3

Qy	545	GCCTCTGGAATCTCTGTGGGCTTCAGAGCTCCGCGCTCCCAAACTGCGCTGCGAAAC	604
Db	943	GCCTCTGGAATCTCTGTGGG--TTCCASITCCGCGCTCCCAAACTGCGCTGCGAAACA	886
Qy	605	ATGCGCACTGTGTGCACTGAACCTGTGCT-CTTGAGCTAGAGATGCTTGGATCCCGG	663
Db	885	ATGCGCACTGTGTGCACTGAACCTGTGCTCTCTGGGCTAGAGATGCTTGTGTTCCCGG	826
Qy	664	CGGAGTACCGGGGCTCTGAGCTGATCTGCACTGGGGGGGCTGCAAGTGTCTCGGGCTCG	723
Db	825	CGGAGTACCGGGGCTCTGAGCTGATCTGCACTGGGGGGGCTGCAAGTGTCTCGGGCTCG	766
Qy	724	GAGCACACTGTGGAAGGCAACCGTTCCTGTGCGAGATCCAGTGTTCACCTCAGACCC	783
Db	765	GAGCACACTGTGGAAGGCAACCGTTCCTGTGCGAGATCCACVABAAAAAAMMAAAMAA	706
Qy	784	GCTTTTGGCAAGTTGAAGAGGCTCTTGGGGGCGCCCGGAGGCGTGTGGCGTGTGGCGCG	843
Db	705	VCCAAACCCAAAGTTGACGAGGCGCTTGGGGGCGCCCGGAGGCGTGTGGCGTGTNNKCMNC	646
Qy	844	TTTCTGAGGAGGGCGCCGGAAGAAAACAGTGCCTATGACAGTTGCTGTCTGCTTGGAA	903
Db	645	TTTCTGAGGAGGCGCCGGAAGAAAACAGTGCCTATGAGCAHTGTCTGTCTGCTTGGAA	586
Qy	904	GAATTCGCTGGAAGAGGCTCAGAGACTCAGGTCCAGAGCTGGAACATATCTGCACTCTG	963
Db	585	GAATTCGCTGGAAGAGGCTCTAGAGACTCAGGTCCAGAGCTGGAACATATCTGCACTCTG	526
Qy	964	CCCTCTGACTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTCAACCGCGCTGTGCC	1022
Db	525	CCCTCTGACTCAGCGCGCTACTTCCAAATATGAGGGGTCTCTGACTCAACCGCGCTGTGCC	466
Qy	1024	CAGGGTGCATCTGGACTGTGTTTAAACAAGACGTATGCTGAGTCTAAGACGCTCCAC	1083

Db	465	CAGGGTGTCACTCTGGA	CTGTGTATTAA	CCAGACAGATGATCTGAGTGTCTAAGCACTTCCAC	406
Qy	1084	ACCTCTCTGACACACC	CTGTGGGGA	CTGTGATCTTCGGCTTAAGCTTAACTTCCAGCG	11443
Db	405	ACCTCTCTGACACACC	TGTGGGGA	CTGTGATCTTCGGCTTAAGCTTAACTTCCAGCG	346
Qy	1144	ACGCAACCTTTGAAT	TGGCGAGTGA	TGAGGCTTCCTTCCTGCTGAGTGA	CAGCAAGT 1203
Db	345	ACGCAAGCTTTGAAT	TGGCGAGTGA	TGAGGCTTCCTTCCTGCTGAGTGA	CAGCAAGT 286
Qy	1204	CTTGGGGCTGTGAG	CCAGTCCAC	TGAACTCTCGCTGGCTGCGTGGAGATCCTAAC	126
Db	285	CTTGGGGCTGTGAG	CCAGTCCAC	TGAACTCTCGCTGGCTGCGTGGAGATCCTAAC	226
Qy	1264	CTGGTTTGTGGCC	CTCTTTTGTCTGTCA	CCAGCGTGGCTTCCTTGTGCAATGAGAAG	13223
Db	225	CTBAHTTTGGCC	CTCTTTTGTCTGTCA	CCAGCTCTCGTTCCTTGTGCAATGAGAAG	166
Qy	1324	CAGCA	CAGAAAGGGGA	CCAAAGGGGGTGTGACTAACCGCCAGCAAGATGACCGAGACT	13833
Db	165	CAGTACAGAAAGGGGA	CCAAAGGGGGTGTG	CTAACCCAGCAAGATGACCGAGACT	107
Qy	1384	GGACCTTAAGAGGCT	TGATCTTGAGAGATGT	TAGAAGCCAGCCAGAGGATCTTGAGGGGGA	14433
Db	106	GGACCTTAAGAGG	GMTKGATCTTGAGAGATGT	TAGAAGCCAGGYBAAGMNTBTGAGGGGGA	47
Qy	1444	GGCGGTAACTGT	CCTGCTGCTCATATA	TGCACTTCCTTTAACT 1489	
Db	46	GGGGGTGANGKCGT	GGCTGSMATATNAT	TGCVAGTTCCTTTAACT 1	

RESULT 15
AL555184

LOCUS	AU555184	927 bp	linear	EST 30-MAR-2004
DEFINITION	A1555184 Homo sapiens HELA CELLS COR 25-NORMALIZED Homo sapiens			
	cDNA clone CS0DK007YK10 5'-PRIME, mRNA sequence.			
ACCESSION	A1555184			
VERSION	A1555184.3	GI:45859924		

FEATURES

BOURCE

